

STUDY clustering overview



STEP 1

Build a STUDY

STEP 2

Precompute the data

STEP 3

Precluster the data

STEP 4

Cluster the data

STEP 5

Edit/view the clusters



STUDY clustering overview



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STEP 4

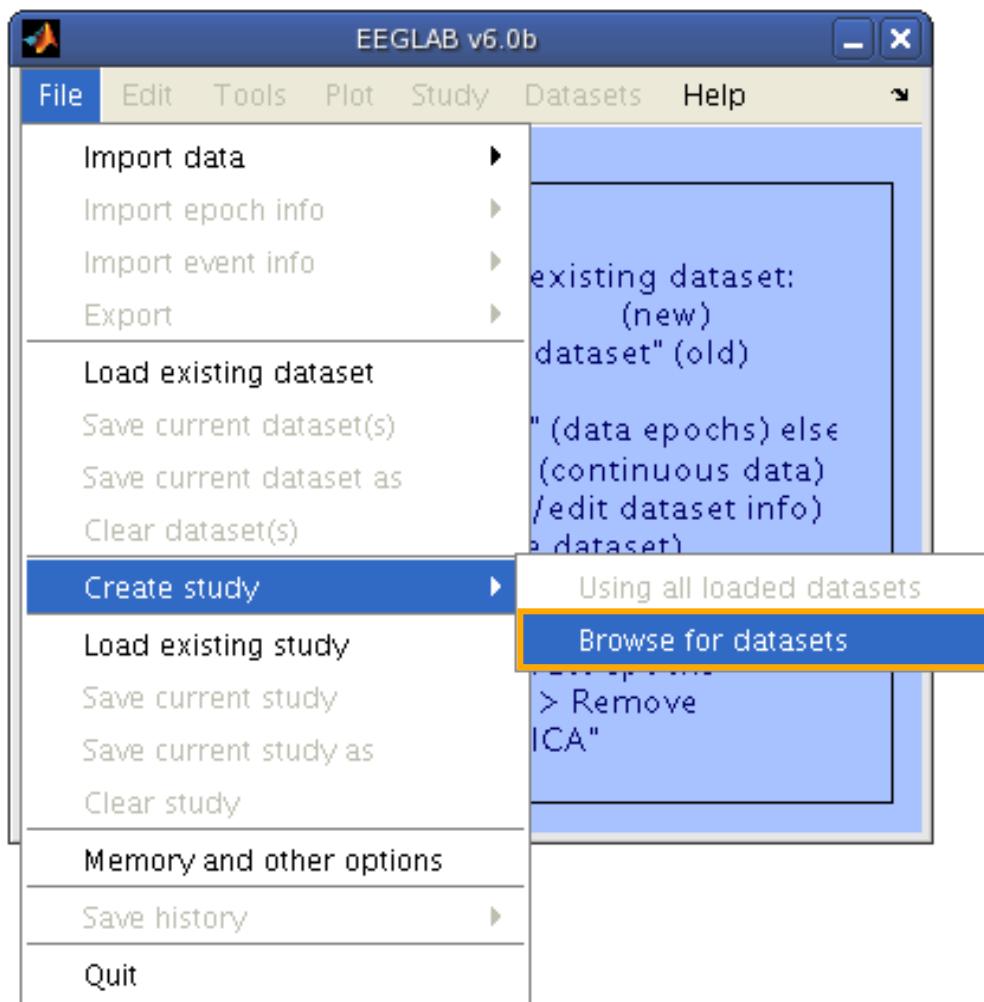
Cluster the data

STEP 5

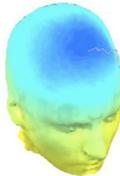
Edit/view the clusters



Build a STUDY



Build a STUDY, cont'd



EEG signal visualization.

Create a new STUDY set -- pop_study()

STUDY set name:

STUDY set task name:

STUDY set notes:

dataset filename:

1	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
2	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
3	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
4	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
5	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
6	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
7	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
8	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
9	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>
10	<input type="text"/>	<input type="button" value="..."/>	<input type="button" value="subject"/>	<input type="button" value="session"/>	<input type="button" value="condition"/>	<input type="button" value="group"/>	<input type="button" value="Select by r.v."/>	<input type="button" value="Clear"/>

Important note: Removed datasets will not be saved before being deleted from EEGLAB memory

Update dataset info – datasets stored on disk will be overwritten (unset =)

Delete cluster information (to allow loading new datasets, set new component)

Save this study to a disk file named:

Choose dataset to add to STUDY -- pop_study()

Look In:

S01_attend1_pos1.set
 S01_attend1_pos5.set
 S01_attend5_pos1.set
 S01_attend5_pos5.set

File Name:
Files of Type:

Edit dataset info

The image shows the EEGLAB software interface. A main window titled "Create a new STUDY set – pop_study()" displays a table of dataset information. An inset window titled "pop_study(): Pre-select components" is overlaid on the main window.

Main Window (Create a new STUDY set – pop_study()):

- Edit STUDY set information:**
 - STUDY set name: (empty)
 - STUDY set task name: (empty)
 - STUDY set notes: (empty)
- Dataset Table:**

	dataset filename	browse	subject	session	condition	group	Select by r.v.
1	IDY/S01/S01_attend1_pos1.set	...	S01	1	TargAttnL	normals	All comp. Clear
2	IDY/S01/S01_attend1_pos5.set	...	S01	1	NONTargAttnL	normals	All comp. Clear
3	IDY/S01/S01_attend5_pos5.set	...	S01	1	TargAttnR	normals	All comp. Clear
4	IDY/S01/S01_attend5_pos1.set	...	S01	1	NONTargAttnR	normals	All comp. Clear
5	IDY/S02/S02_attend1_pos1.set	...	S02	1	TargAttnL	normals	All comp. Clear
6	IDY/S02/S02_attend1_pos5.set	...	S02	1	NONTargAttnL	normals	All comp. Clear
7	IDY/S02/S02_attend5_pos5.set	...	S02	1	TargAttnR	normals	All comp. Clear
8	IDY/S02/S02_attend5_pos1.set	...	S02	1	NONTargAttnR	normals	All comp. Clear
9	IDY/S03/S03_attend1_pos1.set	...	S03	1	TargAttnL	normals	All comp. Clear
10	IDY/S03/S03_attend1_pos5.set	...	S03	1	NONTargAttnL	normals	All comp. Clear
- Important note:** Removed datasets will not be saved before being deleted from EEGLAB memory.
- Page Navigation:** < Page 1 >
- Checkboxes:**
 - Update dataset info – datasets stored on disk will be overwritten (unset = Keep study info separate).
 - Delete cluster information (to allow loading new datasets, set new components for clustering, etc.)
 - Re-save STUDY. Uncheck and use menu File > Save study as to save under a new filename
- Buttons:** Cancel, Help, Ok

Inset Window (pop_study(): Pre-select components):

- Enter maximum residual (topo map – dipole proj.) var. (in %)
15
- NOTE: This will delete any existing component clusters!
- Keep only in-brain dipoles.
- Buttons: Cancel, Help, Ok

ICs to cluster



Create a new STUDY set

STUDY set name: pop_study0

STUDY set task name:

STUDY set notes:

dataset filename

1	objects/S02/syn02-S253-clean.
2	objects/S02/syn02-S254-clean.
3	objects/S05/syn05-S253-clean.
4	objects/S05/syn05-S254-clean.
5	objects/S07/syn07-S253-clean.
6	objects/S07/syn07-S254-clean.
7	objects/S08/syn08-S253-clean.
8	objects/S08/syn08-S254-clean.
9	objects/S10/syn10-S253-clean.
10	objects/S10/syn10-S254-clean.

Important note: Removed datasets will

Update dataset info - datasets

Delete cluster information (to allow loading new datasets, set new components for clustering, etc.)

Save this study to a disk file named:

...

Create a new STUDY set -- pop_study0

select components

ic 19
ic 20
ic 21
ic 22
ic 23
ic 24
ic 25
ic 26
ic 27
ic 28
ic 29
ic 30
ic 31
ic 32

Synonyms
Word Recognition

condition	group	Select by r.v.
Synonyms		<input type="button" value="Comp.: 1 2 ..."/>
on-synonyms		<input type="button" value="Comp.: 1 2 ..."/>
synonyms		<input type="button" value="Comp.: 1 2 ..."/>
on-synonyms		<input type="button" value="Comp.: 1 2 ..."/>
synonyms		<input type="button" value="Comp.: 1 2 ..."/>
on-synonyms		<input type="button" value="Comp.: 1 2 ..."/>
synonyms		<input type="button" value="Comp.: 1 2 ..."/>
on-synonyms		<input type="button" value="Comp.: 1 2 ..."/>
synonyms		<input type="button" value="Comp.: 1 2 ..."/>
on-synonyms		<input type="button" value="Comp.: 1 2 ..."/>
GLAB memory		<input type="button" value="Comp.: 1 2 ..."/>

>

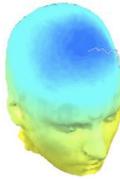
Keep study info separate).

Cancel

Help

Ok

STUDY structure



STUDY =

```
    name: 'Synonyms'  
    task: 'Word Recognition'  
    notes: ''  
    filename: 'workshop.study'  
    cluster: [1x1 struct]  
    history: [1x6654 char]  
    datasetinfo: [1x10 struct]  
    filepath: '/data/STUDY'  
    subject: {'S02' 'S05' 'S07' 'S08' 'S10'}  
    group: {}  
    session: []  
    condition: {'non-synonyms' 'synonyms'}  
    setind: [2x5 double]  
    etc: [1x1 struct]  
    preclust: [1x1 struct]  
    saved: 'no'  
    changgrp: []
```

>>



Subject info in STUDY structure



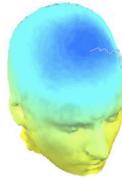
```
>> STUDY.datasetinfo
```

Gives information
for each subject

```
ans =  
1x10 struct array with fields:  
    filepath  
    filename  
    subject  
    session  
    condition  
    group  
    comps  
    index
```

```
>>
```

STUDY clustering overview



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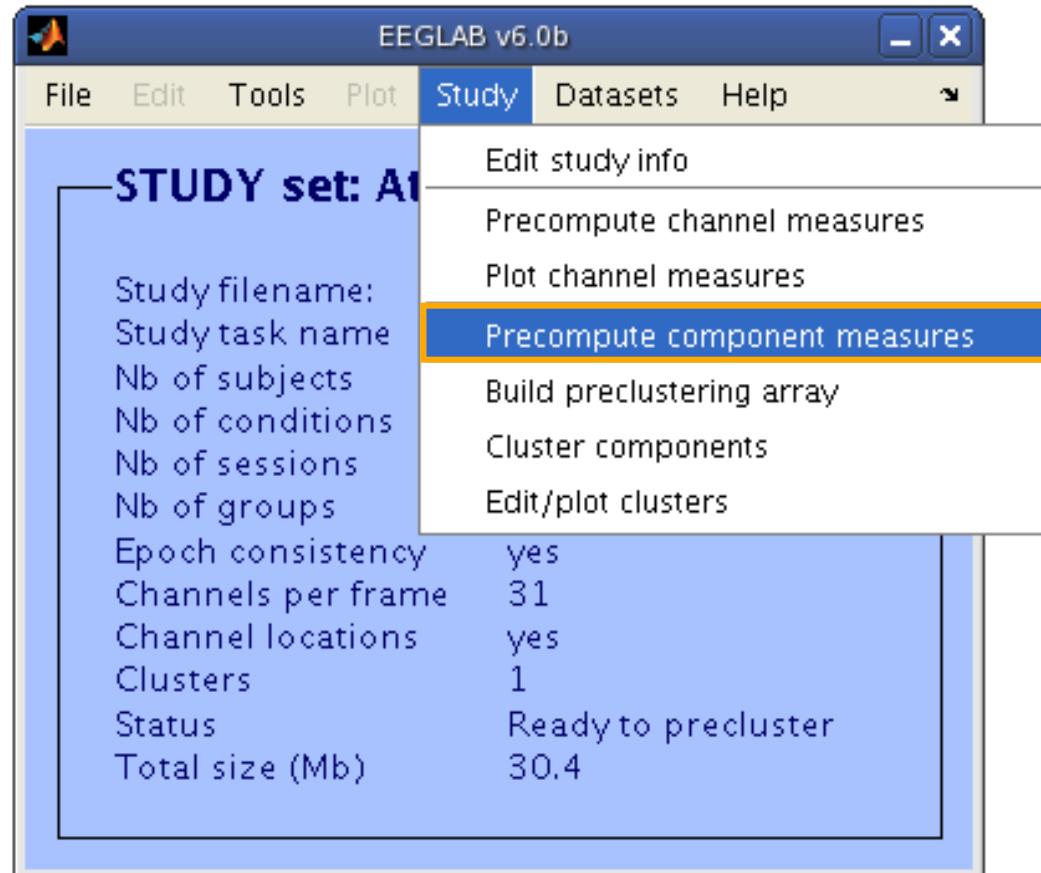
Cluster the data

STEP 5

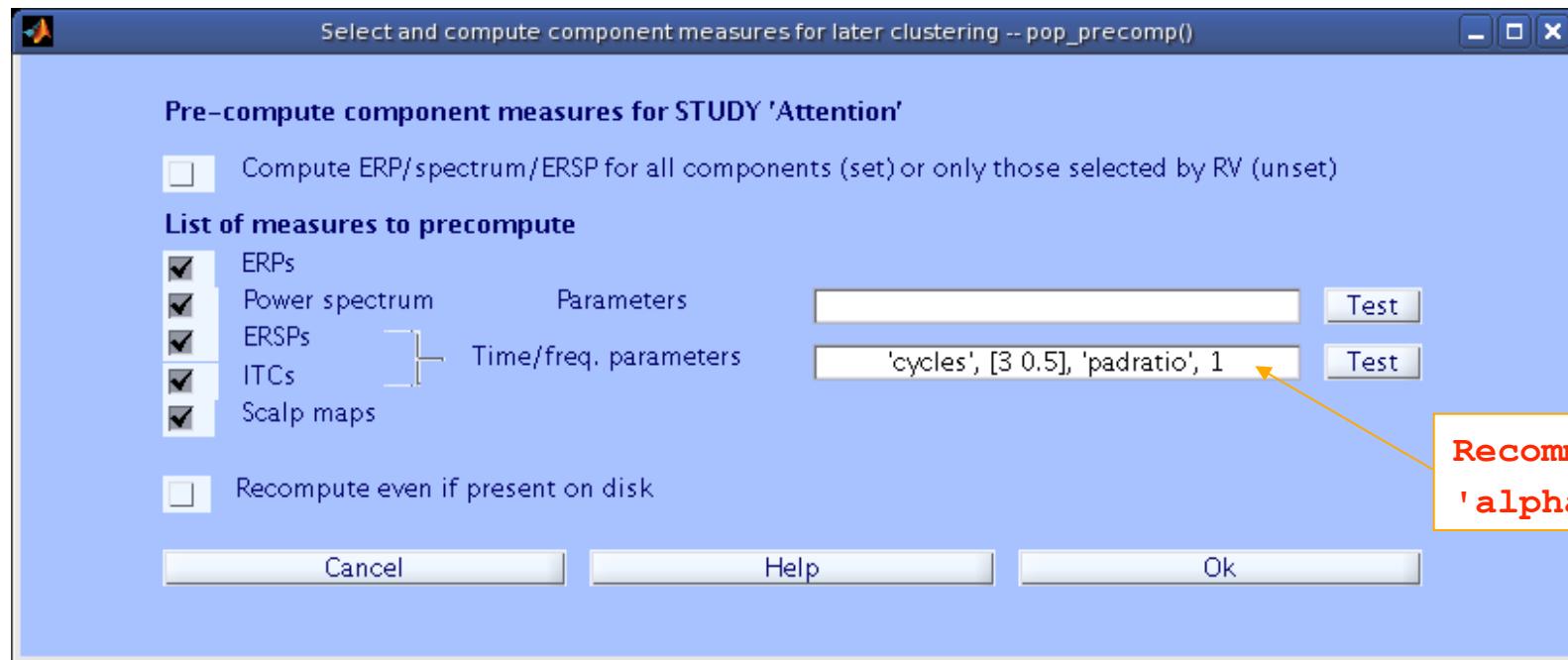
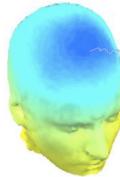
Edit/view the clusters



Precompute data measures



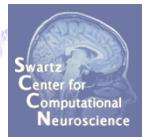
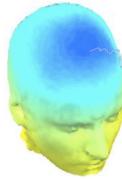
Precompute data measures



**TIP: Compute all measures and so you can
test different combinations for later clustering**



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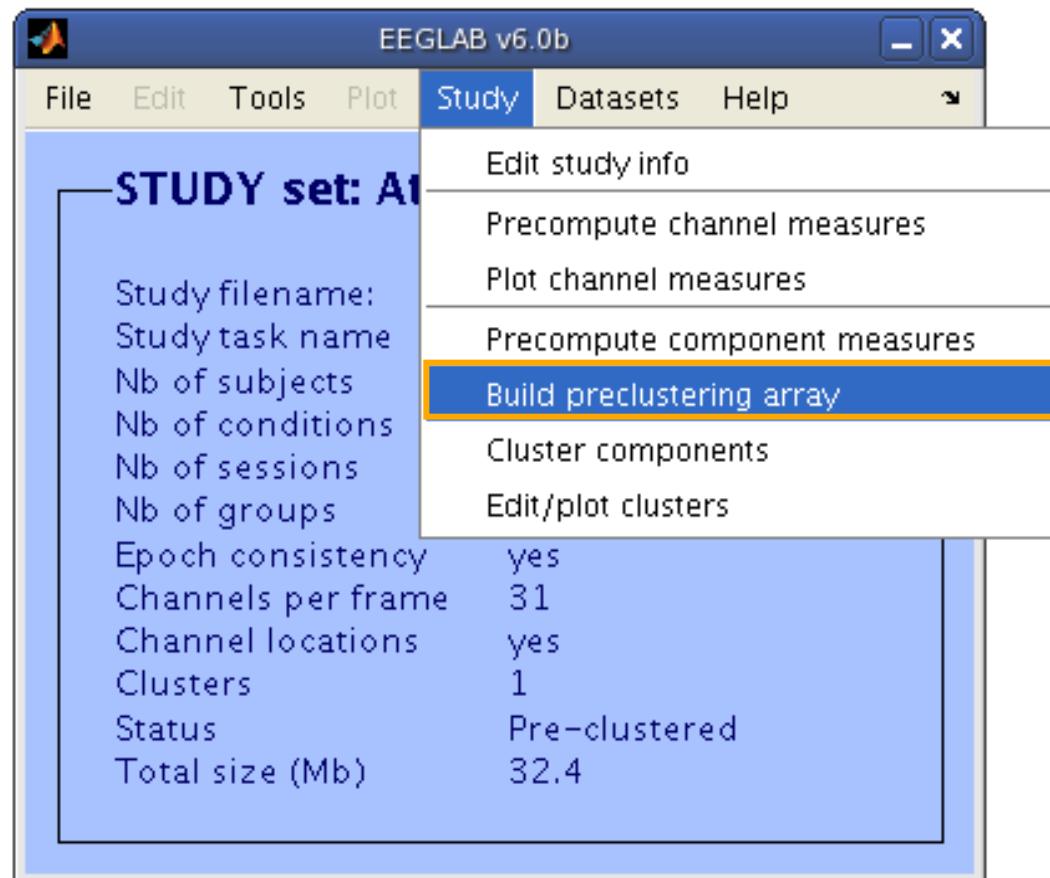
Cluster the data

STEP 5

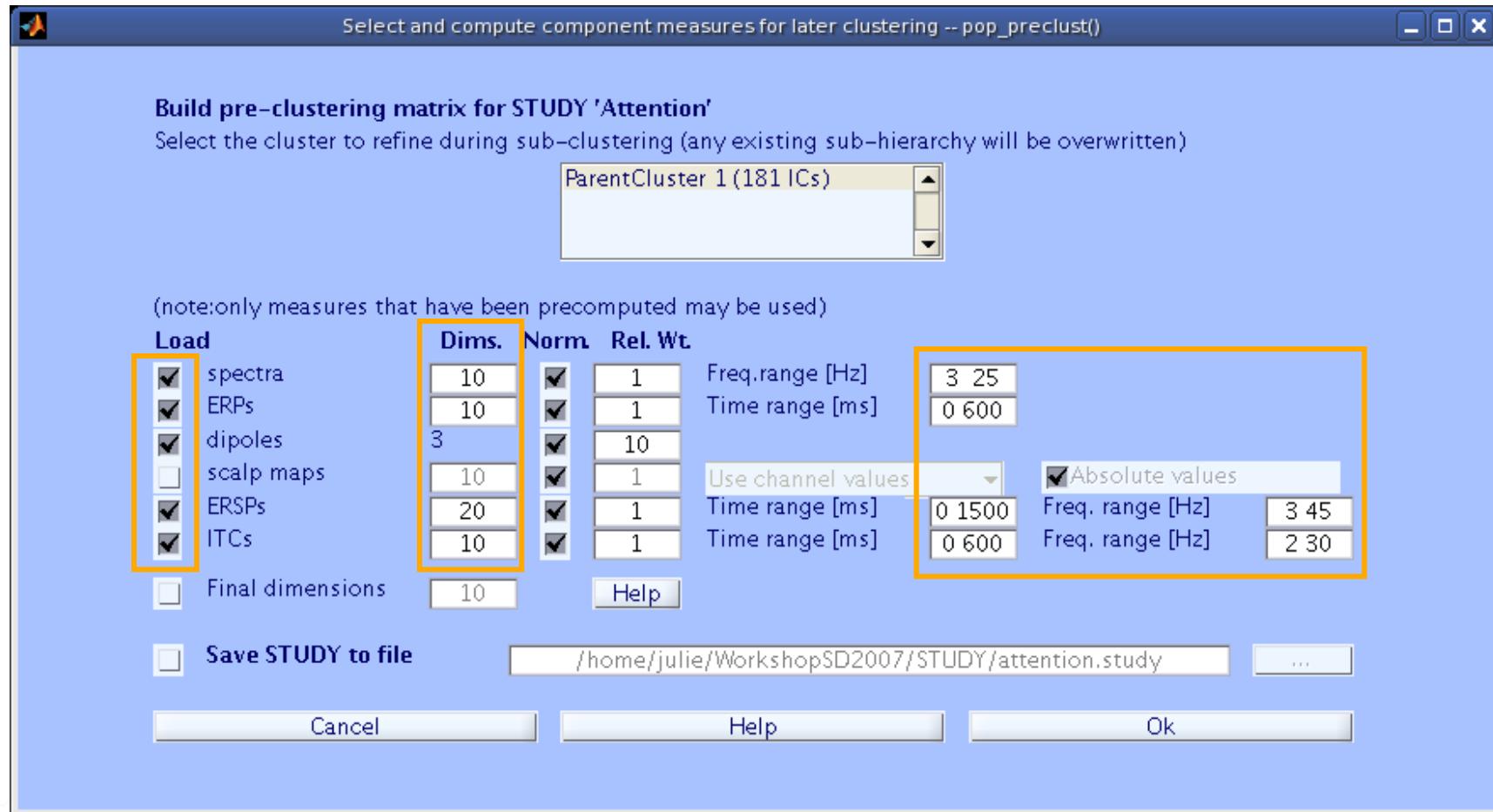
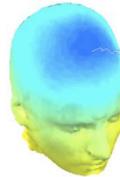
Edit/view the clusters



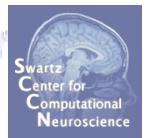
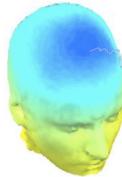
Precluster the data



Precluster the data



STUDY clustering overview



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Cluster the data

STEP 5

Edit/view the clusters



Cluster components



EEGLAB v6.0b

File Edit Tools Plot Study Datasets Help

STUDY set: At

Study filename:
Study task name
Nb of subjects
Nb of conditions
Nb of sessions
Nb of groups
Epoch consistency
Channels per frame
Channel locations
Clusters
Status
Total size (Mb)

yes
31
yes
1
Pre-clust
32.4

Set clustering algorithm -- pop_clust()

Performing clustering on cluster 'ParentCluster 1'

Clustering algorithm: Kmeans

Number of clusters to compute: 12

Separate outliers > [N] std.dev. from any cluster center

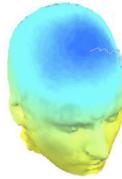
Save STUDY set to disk

Cancel Help Ok

A yellow circle highlights the 'Kmeans' dropdown menu.

Tip: start with a lot of clusters (~25) and work down if necessary

STUDY clustering overview



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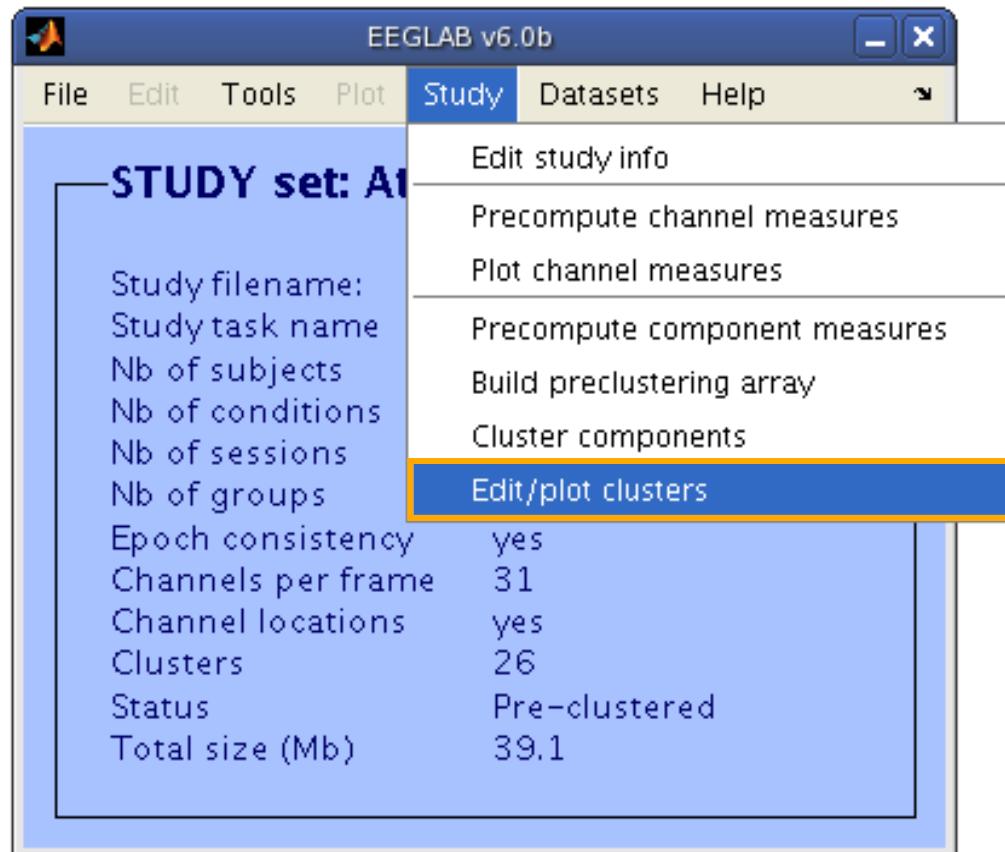
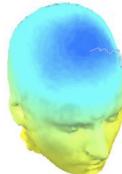
Cluster the data

STEP 5

Edit/view the clusters



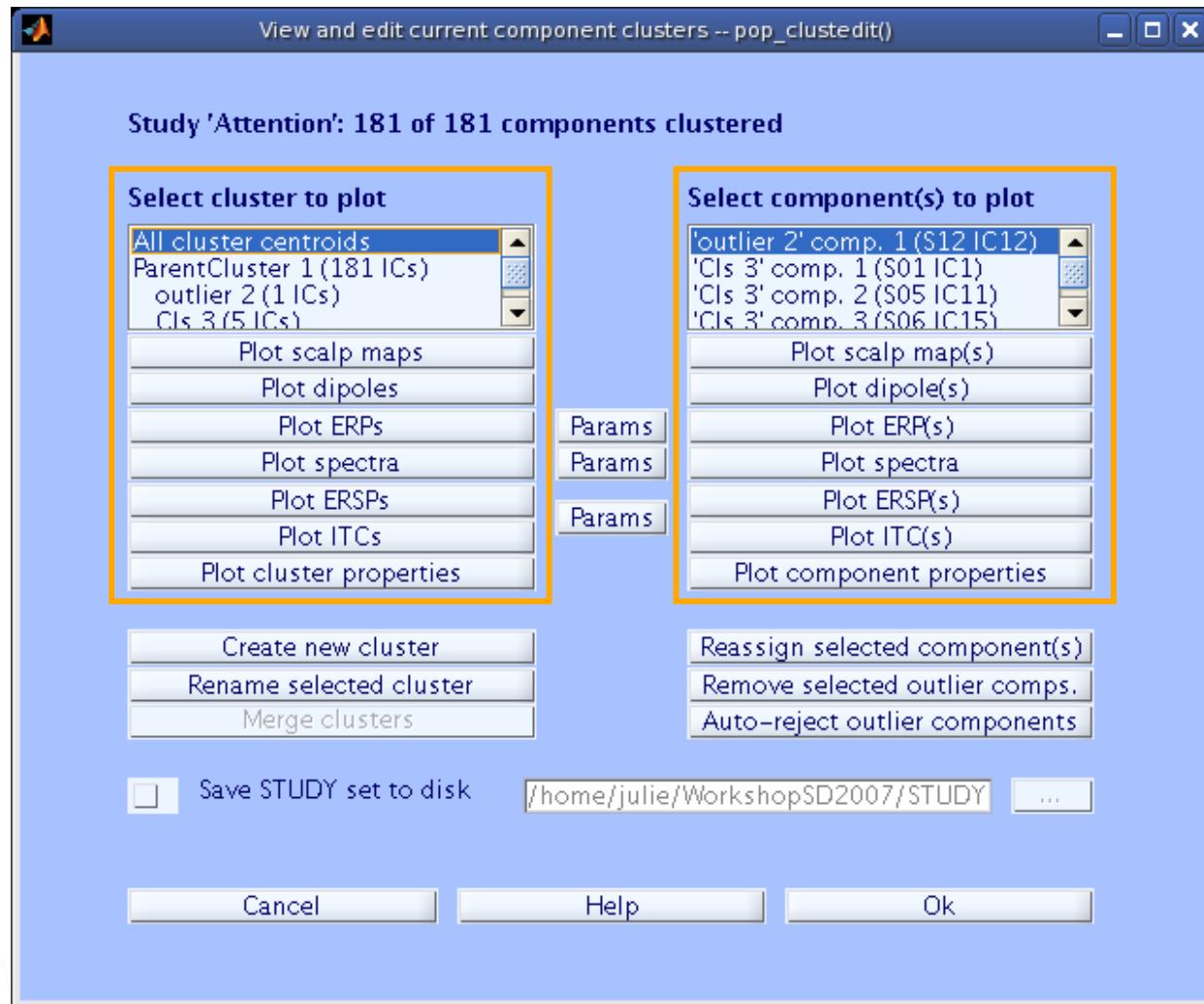
View and edit clusters



View and edit clusters



LEFT SIDE:
Plot measures
of full clusters



Plot cluster data



Study 'Attention': 181 of 181 components clustered

Select cluster to plot

- All cluster centroids
- ParentCluster 1 (181 ICs)
- outlier 2 (1 ICs)
- Cls 3 (5 ICs)
- Plot scalp maps**
- Plot dipoles
- Plot ERPs
- Plot spectra
- Plot ERSPs
- Plot ITCs
- Plot cluster properties

Create new cluster

Rename selected cluster

Merge clusters

Save STUDY set to disk /home/julie

Cancel Help

Select component(s) to plot

- 'outlier 2' comp. 1 (S12 IC12)
- 'Cls 3' comp. 1 (S01 IC1)
- 'Cls 3' comp. 2 (S05 IC11)
- 'Cls 3' comp. 3 (S06 IC15)
- Plot scalp map(s)**
- Plot dipole(s)
- Plot ERP(s)
- Plot spectra

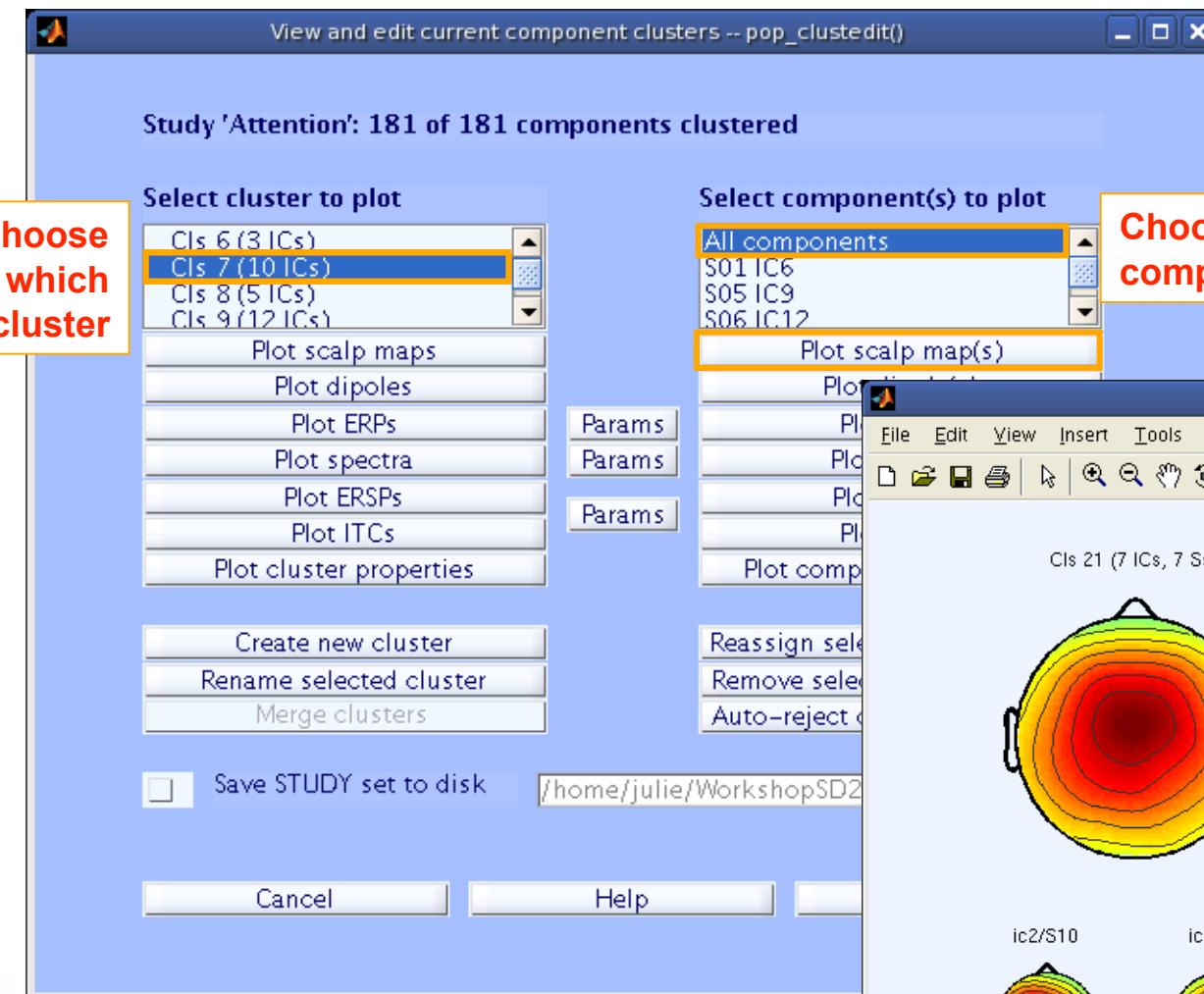
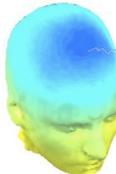
Figure 3: Average scalp map for all clusters

Average scalp map for all clusters

Cluster	ICs	Ss
outlier 2	12	7
Cls 3	4	4
Cls 4	6	8
Cls 5	7	7
Cls 6	3	3
Cls 7	10	6
Cls 8	5	5
Cls 9	12	8
Cls 10	4	4
Cls 11	9	6
Cls 12	3	2
Cls 13	5	4
Cls 14	5	5
Cls 15	14	9
Cls 16	3	3
Cls 17	7	7
Cls 18	4	4
Cls 19	10	8
Cls 20	17	15
Cls 21	6	6
Cls 22	11	8
Cls 23	6	7
Cls 24	7	7
Cls 25	3	3
Cls 26	3	3
Cls 27	1	1

Plot mean scalp maps for easy reference

Plot cluster data



Select component(s) to plot

All components

S01 IC6

S05 IC9

S06 IC12

Plot scalp map(s)

Plot dipoles

Plot ERPs

Plot spectra

Plot ERSPs

Plot ITCs

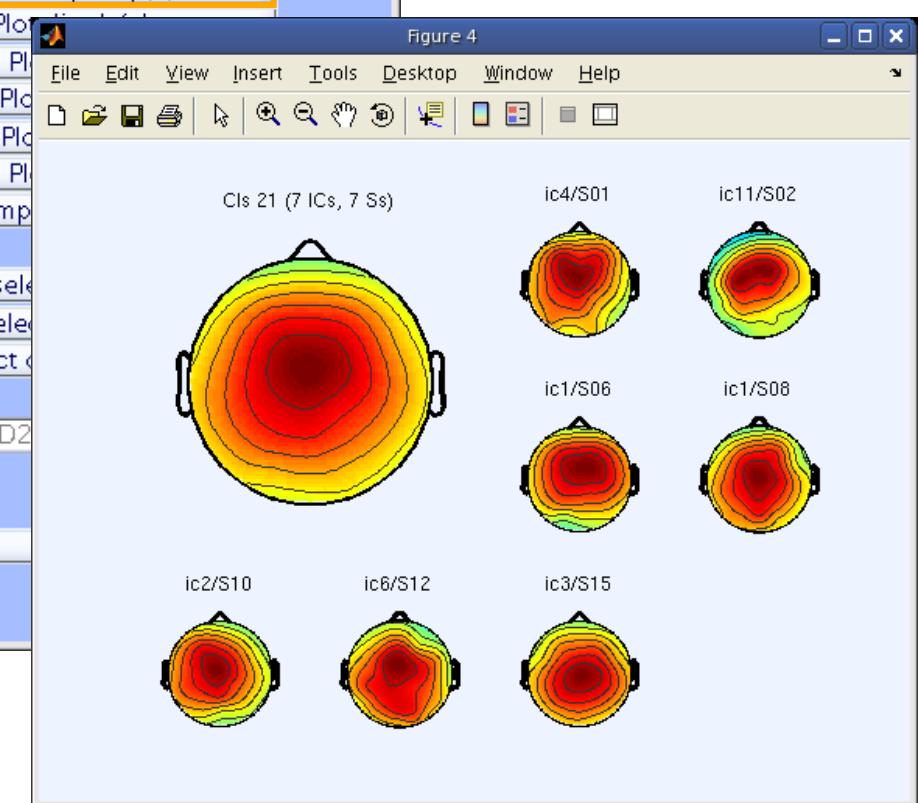
Plot cluster properties

Reassign selected

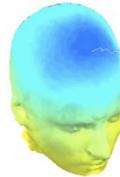
Remove selected

Auto-reject

Choose which components



Plot clusters



View and edit current component clusters -- pop_clustedit()

Study 'Attention': 181 of 181 components clustered

Select cluster to plot

- Cls 6 (3 ICs)
- Cls 7 (10 ICs)**
- Cls 8 (5 ICs)
- Cls 9 (12 ICs)

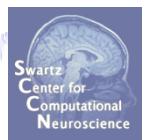
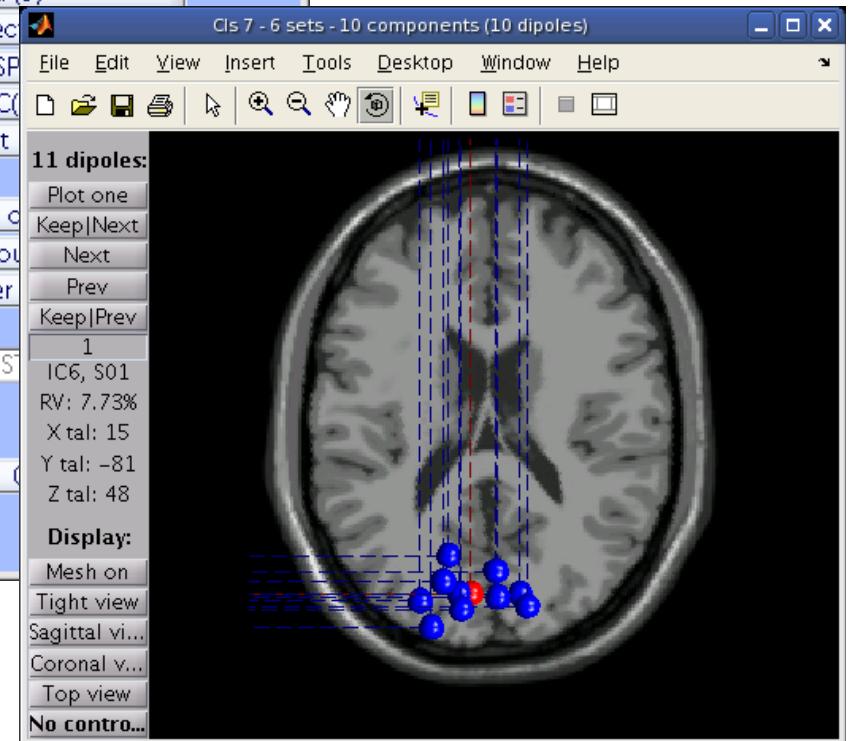
Plot scalp maps
Plot dipoles
Plot ERPs
Plot spectra
Plot ERSPs
Plot ITCs
Plot cluster properties

Params Params Params

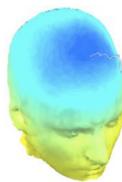
Create new cluster
Rename selected cluster
Merge clusters

Save STUDY set to disk /home/julie/WorkshopSD2007/S

Cancel Help



Plot ERPs



View and edit current component clusters -- pop_clustedit()

Study 'Attention': 181 of 181 components clustered

Select cluster to plot

- Cls 6 (3 ICs)
- Cls 7 (10 ICs)**
- Cls 8 (5 ICs)
- Cls 9 (12 ICs)

Plot scalp maps

Plot dipoles

Plot ERPs

Plot spectra

Plot ERSPs

Plot ITCs

Plot clusters

Create new

Rename selected

Merge

Save STUD

Cancel

Select component(s) to plot

- All components
- S01 IC6
- S05 IC9
- S06 IC12

Plot scalp map(s)

Plot dipole(s)

Plot ERP(s)

Plot spectra

Plot ERSP(s)

Plot ITC(s)

Params

Params

Params

Set parameters for plotting ERPs -- pop_erpparams()

Time range in ms [low high]

Plot scalp map at latency [ms]

Plot limits in uV [low high]

Display filter in Hz [high]

Plot conditions on the same panel

Plot groups on the same panel

Statistics Threshold (p<)

Compute condition statistics

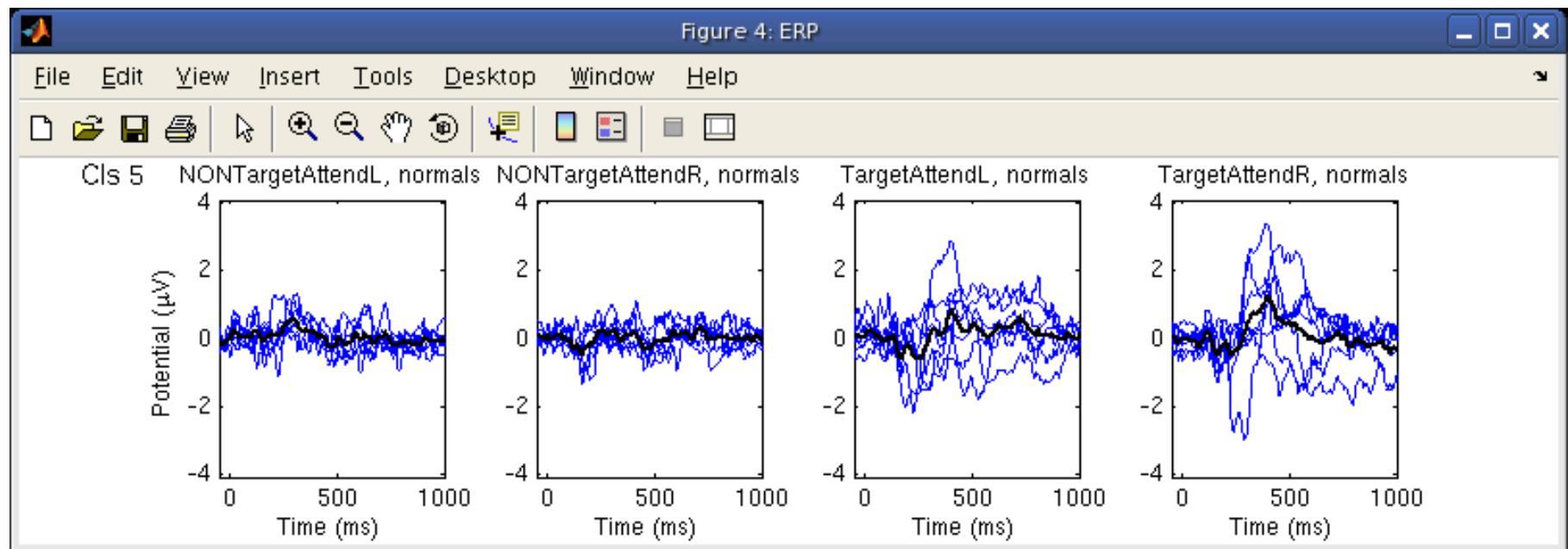
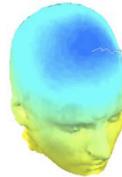
Compute group statistics

Use False Discovery Rate to correct for multiple comparisons

Cancel Help Ok



Plot cluster ERP



Each blue trace is the ERP of a different component



Plot cluster spectra



View and edit current component clusters -- pop_clustedit()

Study 'Attention': 181 of 181 components clustered

Select cluster to plot

- Cls 6 (3 ICs)
- Cls 7 (10 ICs)**
- Cls 8 (5 ICs)
- Cls 9 (12 ICs)

Plot scalp maps

Plot dipoles

Plot ERPs

Plot spectra

Plot ERSPs

Plot ITCs

Plot cluster properties

Create new cluster

Rename selected cluster

Merge clusters

Save STUDY set to disk

Cancel

Select component(s) to plot

- All components
- S01 IC6
- S05 IC9
- S06 IC12

Plot scalp map(s)

Plot dipole(s)

Plot ERP(s)

Plot spectra

Plot ERSP(s)

Plot ITC(s)

Params

Params

Params

Set parameters for plotting specs -- pop_specparams()

Frequency [low_Hz high_Hz]

Plot limits [low high]

Plot scalp map at freq. [Hz] NaN

Subtract individual subject mean spectrum

Plot conditions on the same panel

Plot groups on the same panel

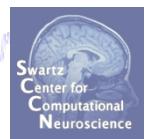
Statistics Threshold (p<=)

Compute condition statistics

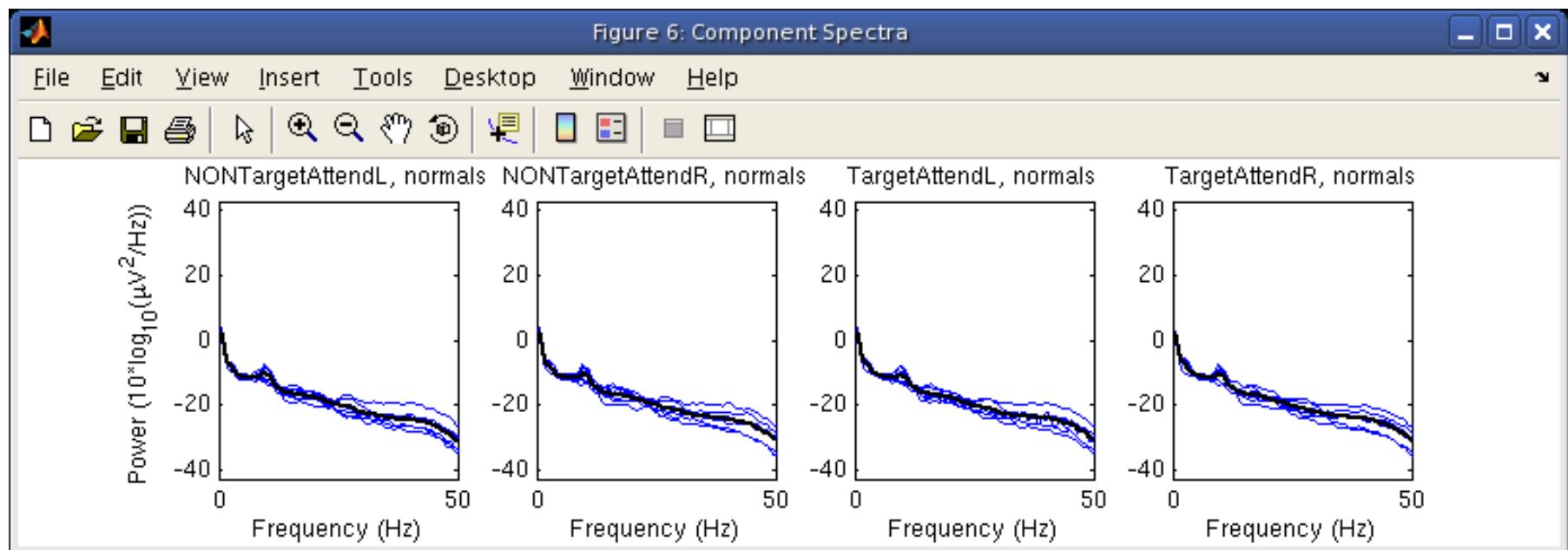
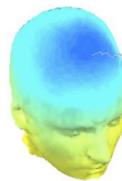
Compute group statistics

Use False Discovery Rate to correct for multiple comparisons

Cancel Help Ok



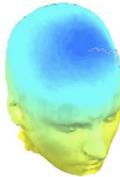
Plot cluster spectra



Each blue trace is the power spectrum of a different component



Plot cluster ERSPs



View and edit current component clusters -- pop_clustedit()

Study 'Attention': 181 of 181 components clustered

Select cluster to plot

- Cls 6 (3 ICs)
- Cls 7 (10 ICs)**
- Cls 8 (5 ICs)
- Cls 9 (12 ICs)

Plot scalp maps
Plot dipoles
Plot ERPs
Plot spectra
Plot ERSPs
Plot ITCs
Plot cluster properties

Create new cluster
Rename selected cluster
Merge clusters
 Save STUDY set to disk

Cancel

Select component(s) to plot

- All components
- S01 IC6
- S05 IC9
- S06 IC12

Plot scalp map(s)
Plot dipole(s)
Plot ERP(s)
Plot spectra
Plot ERSP(s)
Plot ITC(s)

Params

Params

Params

Set ERSP | ITC plotting parameters -- pop_erspparams()

Time range in ms [Low High]
Freq. range in Hz [Low High]
Power limits in dB [Low High] ITC limit (0-1) [High]

Compute ERSP baseline across conditions

Statistics Permutation Threshold (p<)
 Compute condition statistics
 Compute group statistics
 Mask non-significant data (only when threshold is set)
 Use False Discovery Rate to correct for multiple comparisons

Cancel Help Ok



Plot cluster ERSPs

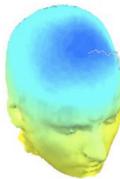
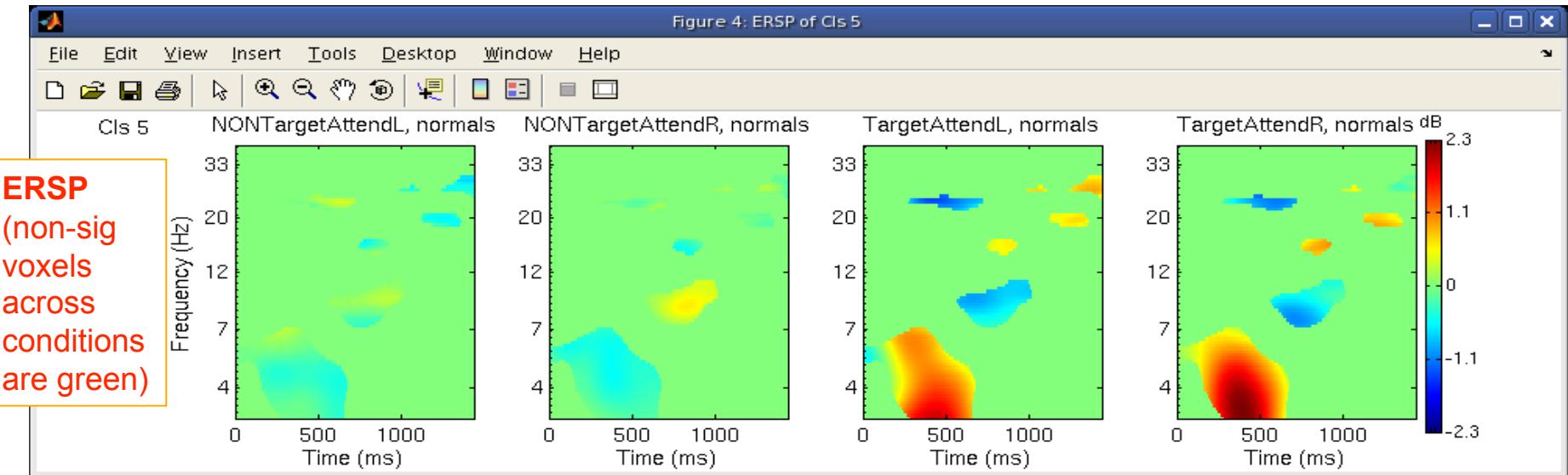
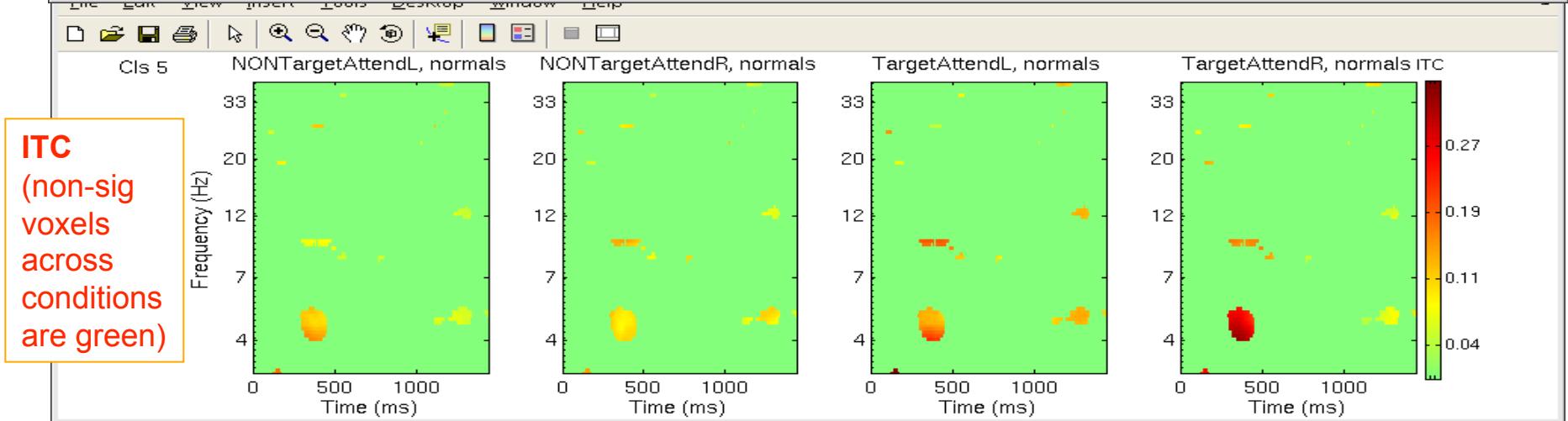


Figure 4: ERSP of Cls 5

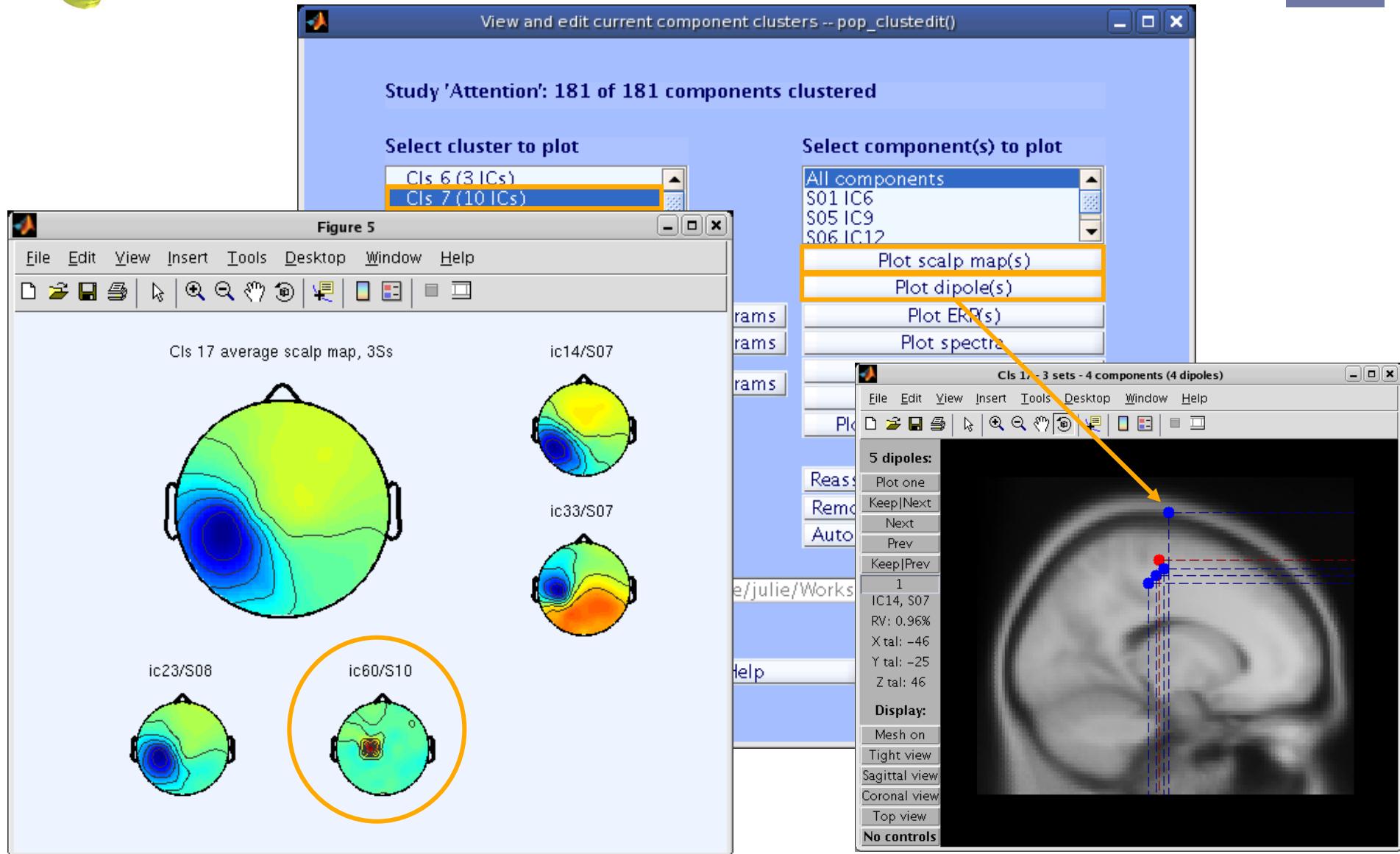
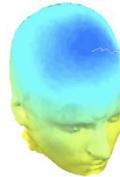
ERSP
(non-sig
voxels
across
conditions
are green)



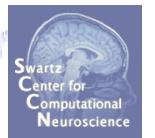
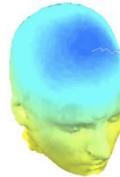
ITC
(non-sig
voxels
across
conditions
are green)



Remove outlier components



Remove outlier components



Study ": 151 of 151 components clustered

Select cluster to plot

- Cls 13 (5 ICs)
- Cls 14 (11 ICs)
- Cls 15 (8 ICs)
- Cls 16 (6 ICs)
- Cls 17 (4 ICs)

Plot scalp maps

Plot dipoles

Plot ERPs

Plot spectra

Plot ERSPs

Plot ITCs

Plot cluster properties

Create new cluster

Rename selected cluster

Merge clusters

Save STUDY set to disk

/home/julie/workshop06/5subjects/WSstudy.study ...

Select component(s) to plot

- All components
- S07 IC14
- S07 IC33
- S08 IC23
- S10 IC60

Plot scalp map(s)

Remove outliers - from pop_clustedit()

Remove currently selected component below from Cls 17 to its outlier cluster?

S10 IC60

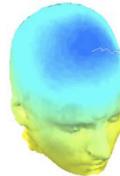
Cancel Ok

Remove selected outlier comps. Auto-reject outlier components

Cancel Help Ok

A modal dialog box titled "Remove outliers - from pop_clustedit()" is displayed in the center. It contains a question "Remove currently selected component below from Cls 17 to its outlier cluster?" followed by the text "S10 IC60". At the bottom are "Cancel" and "Ok" buttons. Below the dialog, there are two additional buttons: "Remove selected outlier comps." and "Auto-reject outlier components".

Remove outlier components



Study ": 151 of 151 components clustered

Select cluster to plot

- Cl 16 (6 ICs)
- Cl 17 (3 ICs)
- Cl 18 (11 ICs)
- Cl 19 (14 ICs)
- Outliers Cls 17 20 (1 ICs)

Plot scalp maps

Plot dipoles

Plot ERPs

Plot spectra

Plot ERSPs

Plot ITCs

Plot cluster properties

Params

Params

Params

Select component(s) to plot

- All components
- S10 IC60

Plot scalp map(s)

Plot dipole(s)

Plot ERP(s)

Plot spectra

Plot ERSP(s)

Plot ITC(s)

Plot component properties

Create new cluster

Rename selected cluster

Merge clusters

Reassign selected component(s)

Remove selected outlier comps.

Auto-reject outlier components

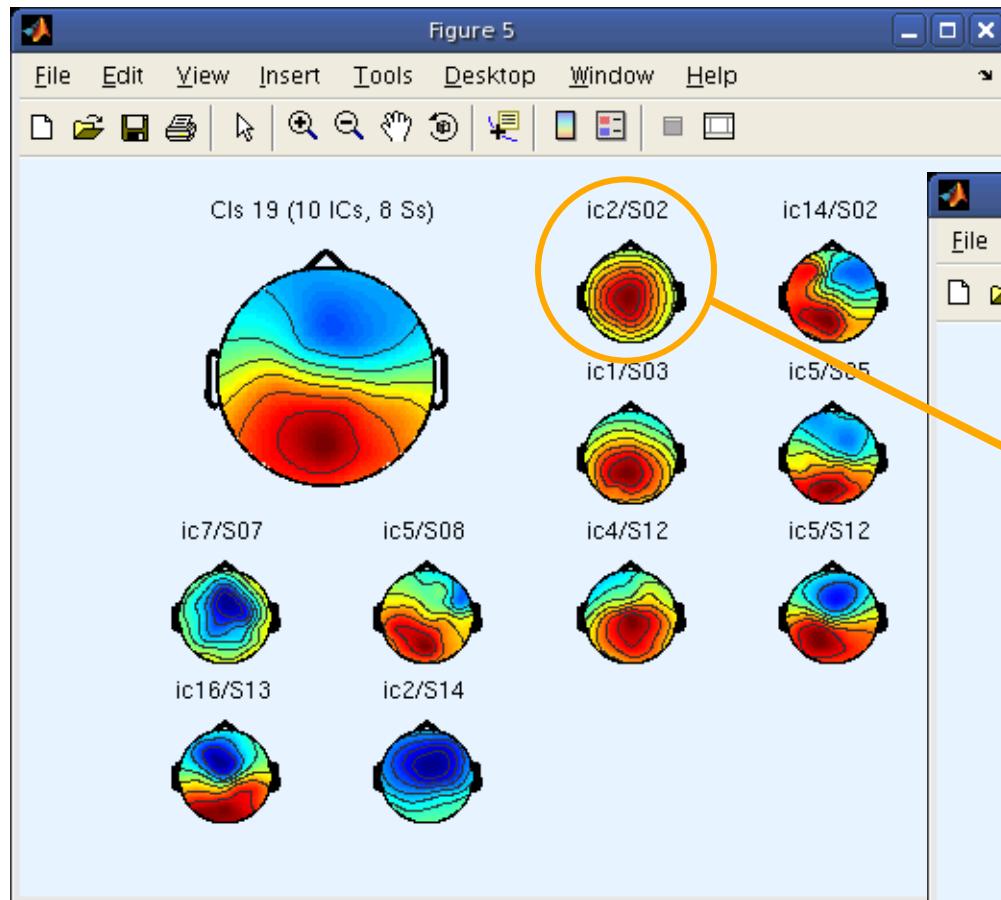
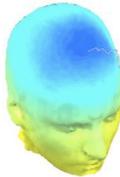
Save STUDY set to disk

/home/julie/workshop06/5subjects/WSstudy.study

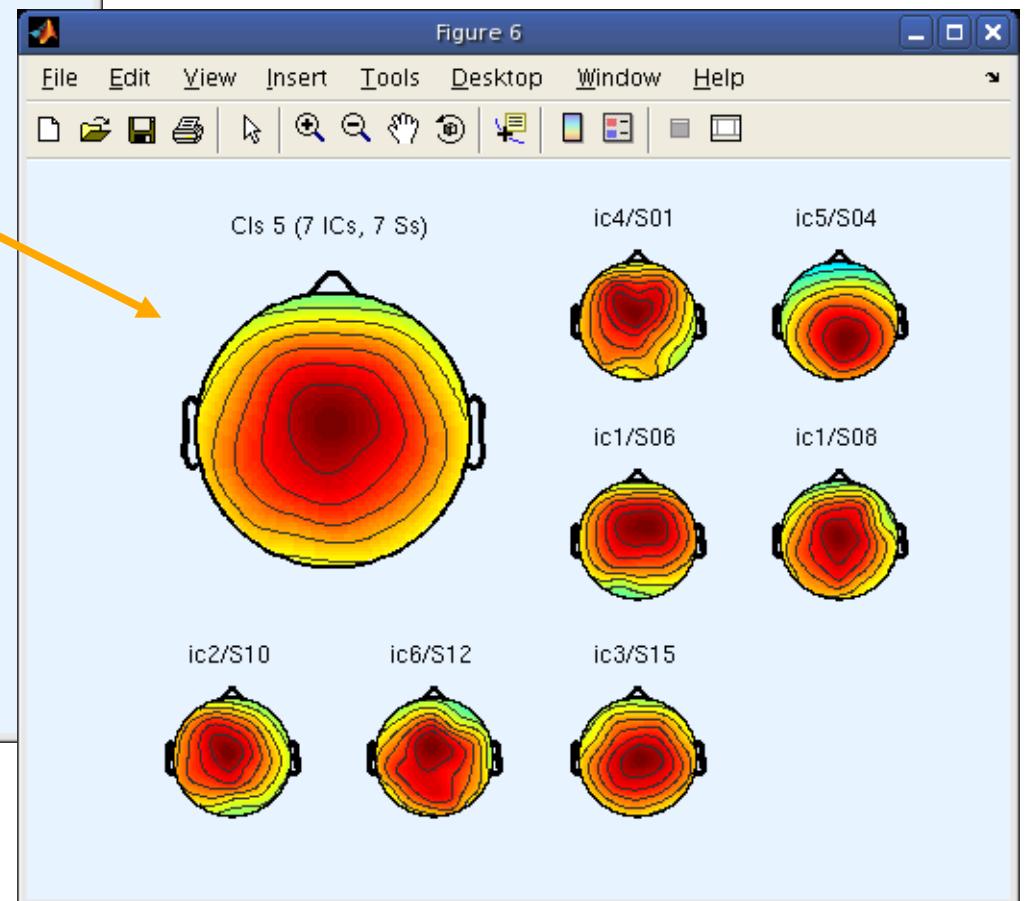
Cancel Help Ok

The screenshot shows a MATLAB graphical user interface titled "View and edit current component clusters -- pop_clustedit()". The window displays two main lists: "Select cluster to plot" on the left and "Select component(s) to plot" on the right. Both lists have orange circles around them, likely indicating they are the focus of the current step. The "Select cluster to plot" list contains several entries: Cl 16 (6 ICs), Cl 17 (3 ICs), Cl 18 (11 ICs), Cl 19 (14 ICs), and Outliers Cls 17 20 (1 ICs). Below this list are buttons for "Plot scalp maps", "Plot dipoles", "Plot ERPs", "Plot spectra", "Plot ERSPs", "Plot ITCs", and "Plot cluster properties", each with a corresponding "Params" button. The "Select component(s) to plot" list contains All components and S10 IC60, also with a "Params" button below it. At the bottom of the window are buttons for "Create new cluster", "Rename selected cluster", "Merge clusters", "Reassign selected component(s)", "Remove selected outlier comps.", and "Auto-reject outlier components". On the left, there is a "Save STUDY set to disk" button with a file path: /home/julie/workshop06/5subjects/WSstudy.study. At the bottom are standard "Cancel", "Help", and "Ok" buttons. A small 3D head model and a brain activity visualization are visible in the top corners of the slide.

Reassign component



If you want to manually reassign
a component to another cluster...



Reassign component



View and edit current component clusters -- pop_clustedit()

Study 'Attention': 181 of 181 components clustered

Select cluster to plot

- Cls 18 (4 ICs)
- Cls 19 (10 ICs) **(highlighted)**
- Cls 20 (17 ICs)
- Cls 21 (6 ICs)

Plot scalp maps
Plot dipoles
Plot ERPs
Plot spectra
Plot ERSPs
Plot ITCs
Plot cluster properties

Params Params Params

Create new cluster
Rename selected cluster
Merge clusters

Save STUDY set to disk /home/julie/WorkshopSD2007/STUDY ...

Cancel Help Ok

Select component(s) to plot

- All components
- S02 IC2
- S02 IC14
- S03 IC1

Plot scalp map(s)
Plot dipole(s)
Plot ERP(s)
Plot spectra
Plot ERSP(s)
Plot ITC(s)
Plot component properties

Reassign selected component(s)
Remove selected outlier comps.
Auto-reject outlier components

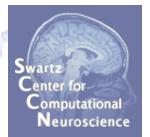
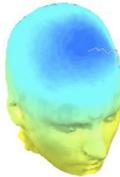
Reassign cluster - from pop_clustedit()

Reassign currently selected component from Cls 19 to the cluster selected below

- Cls 4
- Cls 5
- Cls 6
- Cls 7

Cancel Ok

Reassign component



View and edit current component clusters -- pop_clustedit()

Study 'Attention': 181 of 181 components clustered

Select cluster to plot

- Cl5 4 (8 ICs)
- Cl5 5 (8 ICs) **Selected**
- Cl5 6 (3 ICs)
- Cl5 7 (10 ICs)

Plot scalp maps
Plot dipoles
Plot ERPs
Plot spectra
Plot ERSPs
Plot ITCs
Plot cluster properties

Params Params Params

Create new cluster
Rename selected cluster
Merge clusters

Save STUDY set to disk /home/julie/WorkshopSD2007/

Cancel Help

Select component

- All components
- S01 IC4
- S02 IC2 **Selected**
- S04 IC5

Plot scalp maps
Plot dipoles
Plot ERPs
Plot spectra
Plot ERSPs
Plot ITCs
Plot component

Reassign selected
Remove selected
Auto-reject outliers

Successful reassignment

Figure 7

Cl5 5 (8 ICs, 8 Ss) IC4/S01 ic2/S02

ic5/S04 ic1/S06

ic1/S08 ic2/S10 ic6/S12 ic3/S15

Rename a cluster



Name your cluster of interest

Study 'Attention': 181 of 181 components clustered

Select cluster to plot

- Cl5 4 (8 ICs)
- Cl5 5 (8 ICs)**
- Cl5 6 (3 ICs)
- Cl5 7 (10 ICs)

Plot scalp maps
Plot dipoles
Plot ERPs
Plot spectra
Plot ERSPs
Plot ITCs
Plot cluster properties

Create new cluster
Rename selected cluster
Merge clusters

Save STUDY set to disk /home/julie/WorkshopSD2007/

Select component

- All components
- S01 IC4
- S02 IC2
- S04 IC5

Figure 7

Rename cluster

Mid-central

Ok

Cancel

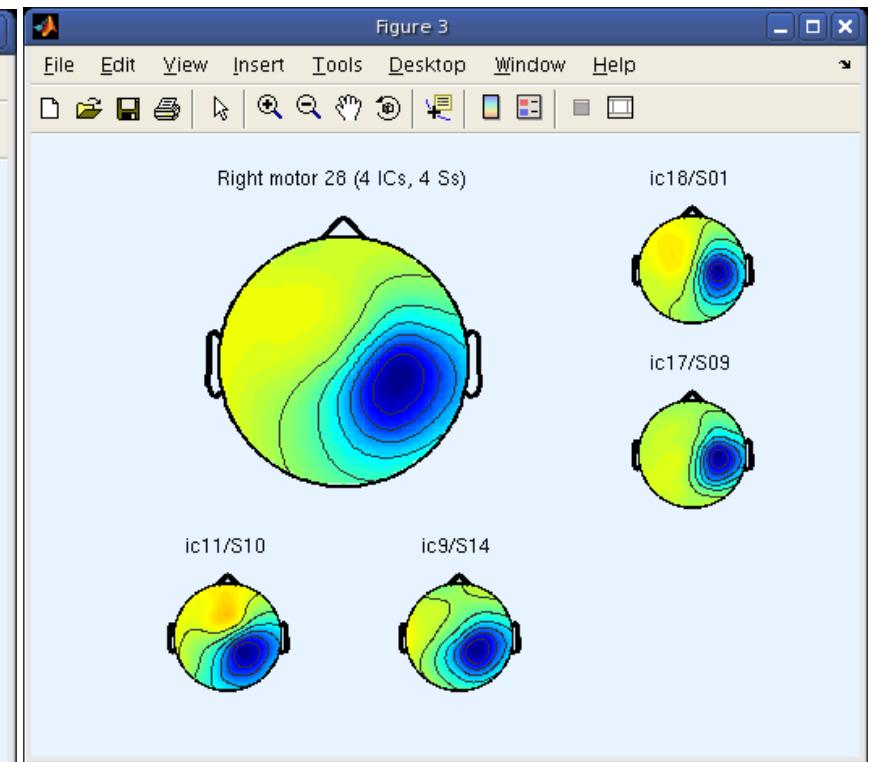
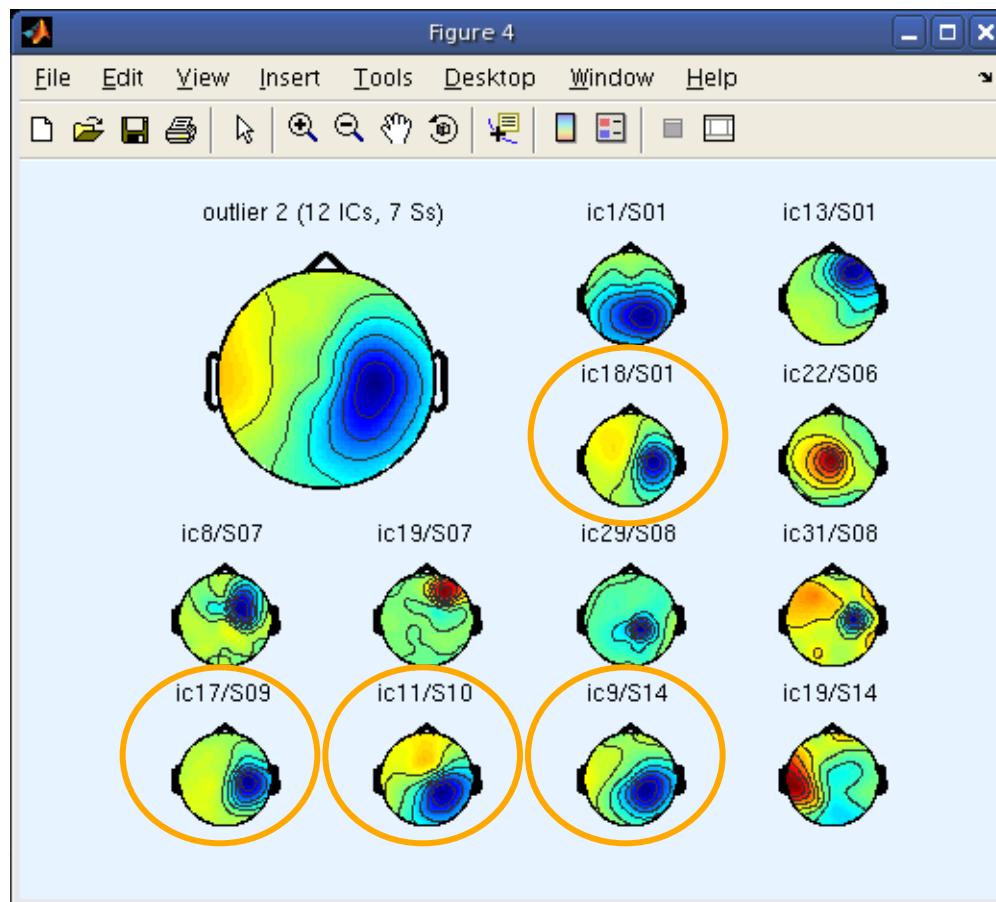
Remove selected cluster
Auto-reject outliers

Scalp maps showing clusters: Cl5 5 (8 ICs, 8 Ss), ic4/S01, ic2/S02, ic5/S04, ic1/S06, ic1/S08, ic2/S10, ic6/S12, ic3/S15.

Create a new cluster

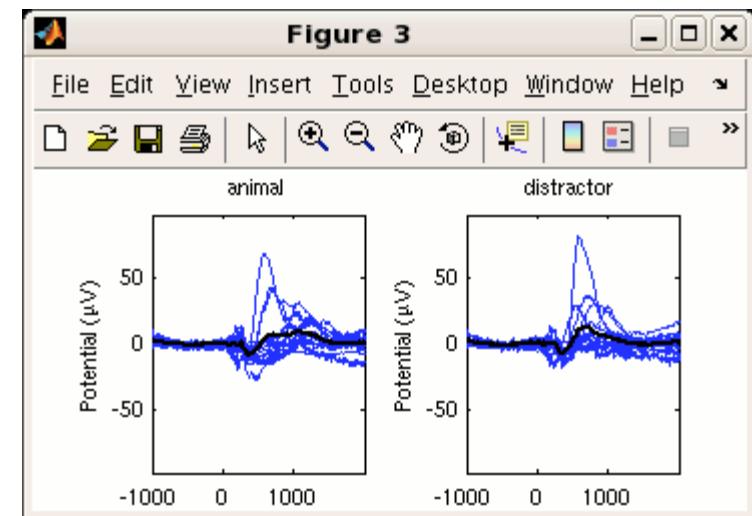
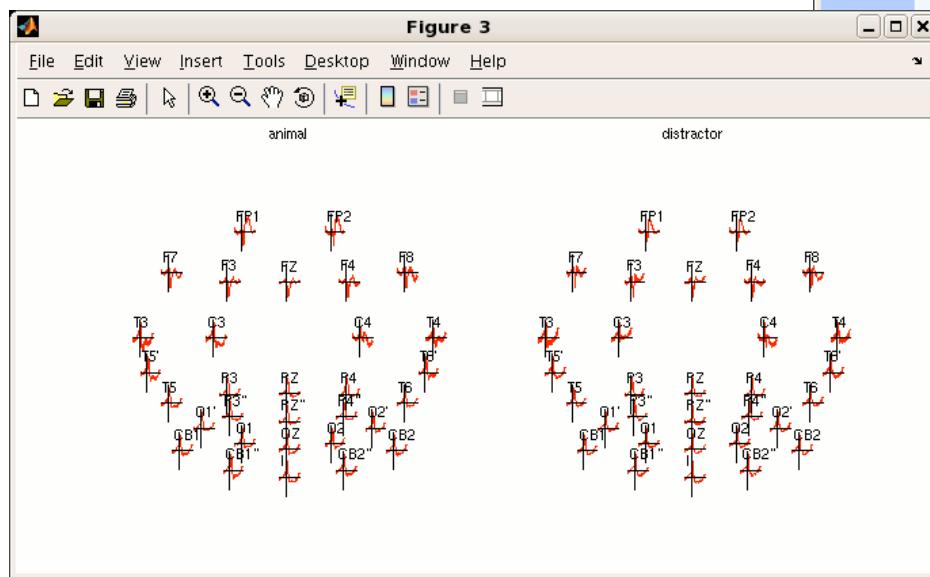
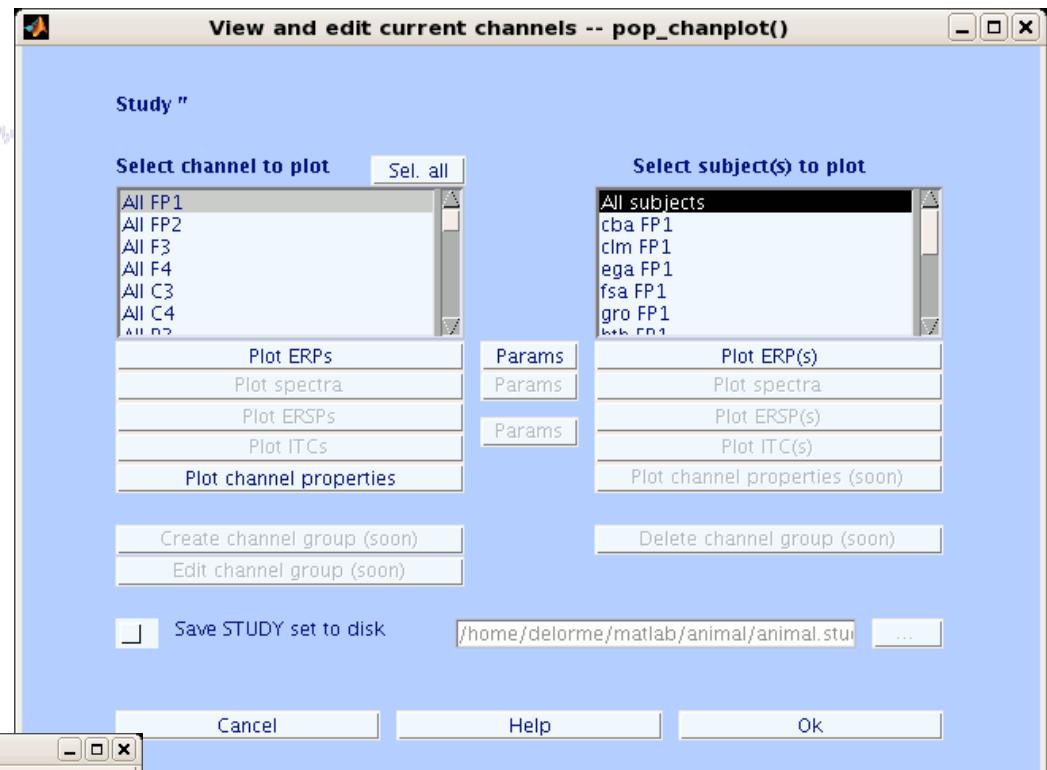
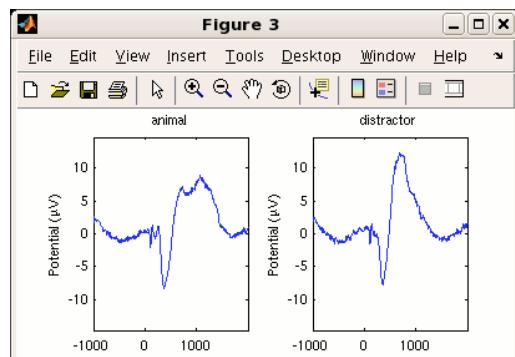


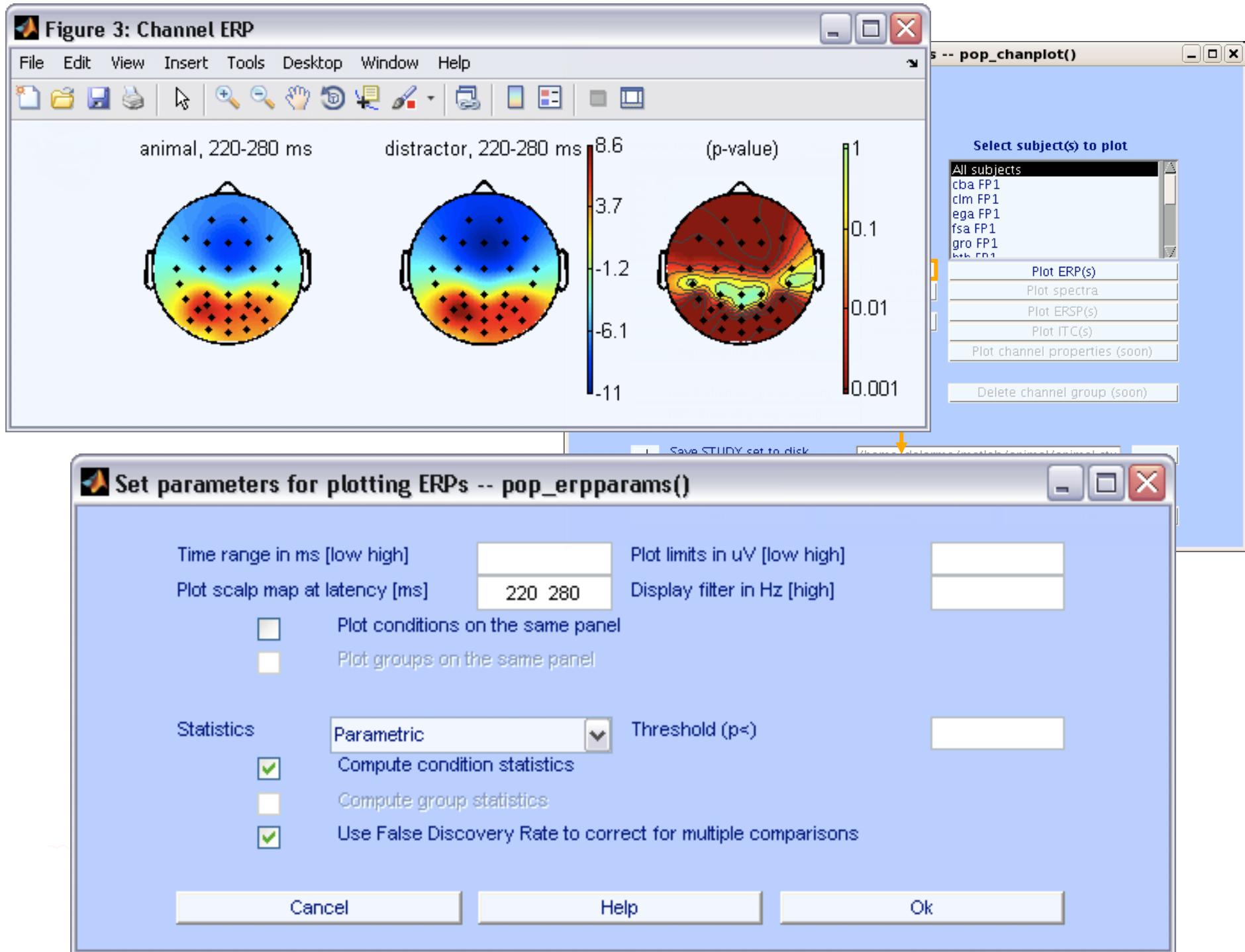
You found a bunch of 'outliers' that seem well-matched



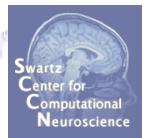
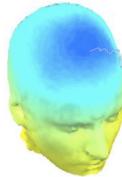
Create a new cluster...

Channel plotting





Exercise



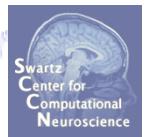
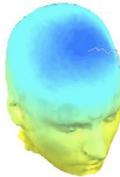
- **Novice**

- Use the GUI to build a STUDY (for practice, try just a few subjects).
- Choose 'precompute' options (but do not recalculate for the sake of time).
- Choose 'precluster' options and cluster.
- Use the GUI to plot cluster and component data using default parameters

- **Intermediate**

- Create a Study and add a single subject. Get the history from the command line and script a loop to build a STUDY with all subjects from the commandline
- Precluster (pre-computation already done) and cluster components using measures of your choice.
- Use the GUI to plot cluster and component data trying out different plotting parameters such as x/y-axis limits, and color scale limits to compare absolute values across clusters.
- Apply statistical thresholds of your choice
- Create and name a new cluster, fill with your choice of ICs

STUDY analysis, Part 1



Task 1

Script STUDY plotting functions

Task 2

STUDY structure details

Task 3

Load/plot data from commandline

Task 4

Apply significance limits

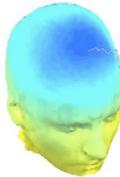
Task 5

Time/frequency analysis within cluster

Exercise...



STUDY analysis, Part 1



Task 1

Script STUDY plotting functions

Task 2

STUDY structure details

Task 3

Load/plot data from commandline

Task 4

Apply significance limits

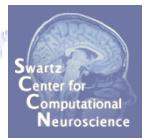
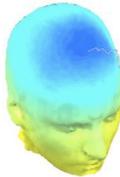
Task 5

Time/frequency analysis within cluster

Exercise...



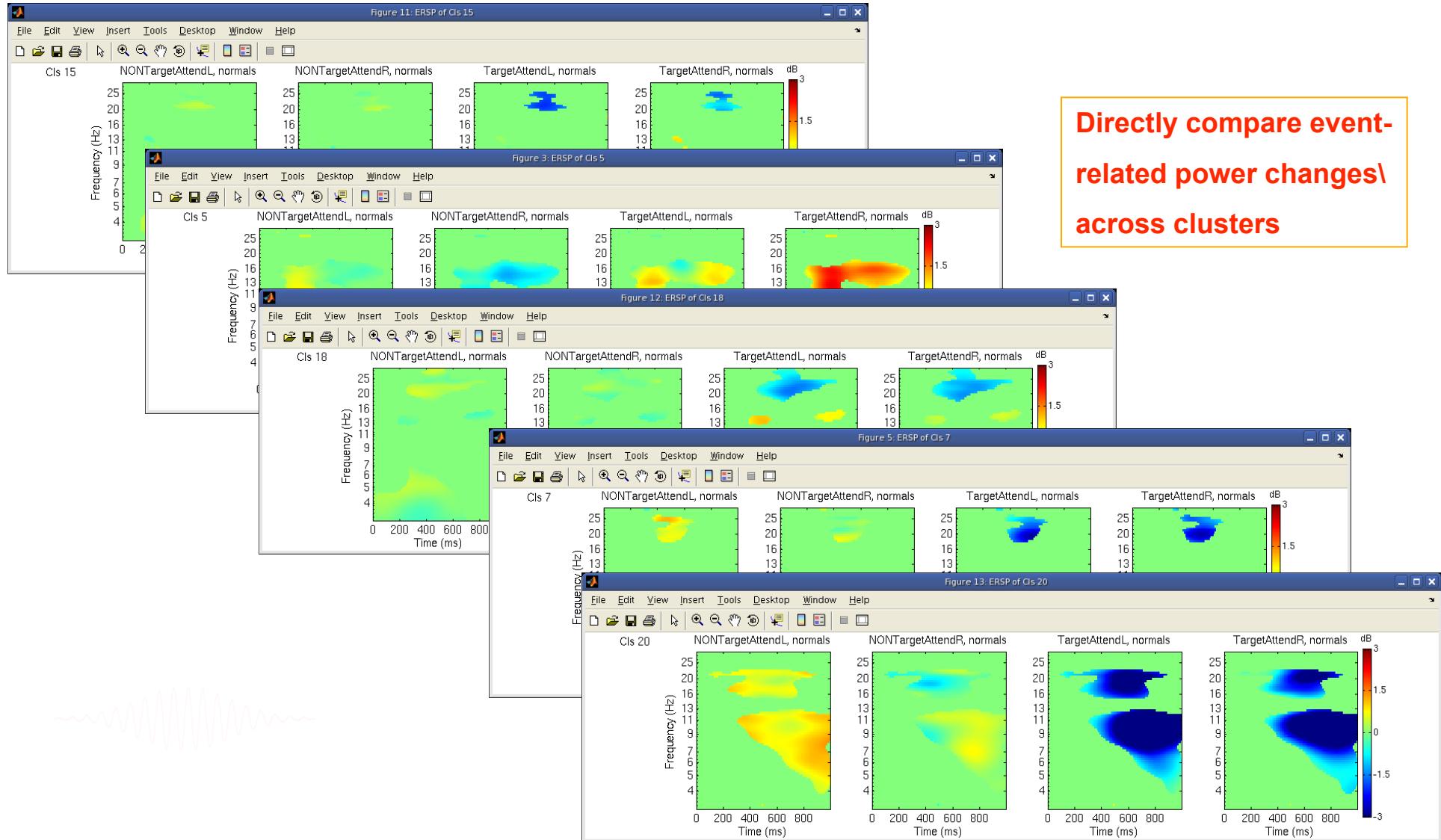
Task 1: Plot cluster ERSP



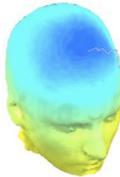
```
% plot all cluster ERSPs with variable parameters using a for  
% loop to compare power across clusters:-----  
  
% Define variables:-----  
frqlim = [3 30]; % ERSP freq range (Hz)  
tmlim = [0 1000]; % ERSP time range (ms)  
maxdb = 4; % set color limit for dB power from baseline  
%-----  
  
for clust = 3:length(STUDY.cluster)  
    STUDY = std_erspplot(STUDY, ALLEEG, 'clusters', clust, ...  
    'plotsubjects', 'on', 'statistics', 'perm', ...  
    'timerange', tmlim, 'freqrange', frqlim, 'threshold', 0.01, ...  
    'ersplim', [-maxdb maxdb]);  
end;
```



Task 1: Cluster ERSP plotting



STUDY analysis, Part 1



Task 1

Script STUDY plotting functions

Task 2

STUDY structure details

Task 3

Load/plot data from commandline

Task 4

Apply significance limits

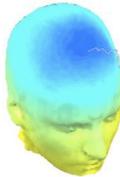
Task 5

Time/frequency analysis within cluster

Exercise...



Task 2: STUDY structure details



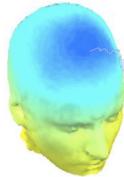
Question:

I want to know which **ICs** from which
subjects are in a particular **cluster**.

Where in the **STUDY structure** can I find this information?



Task 2: Understanding STUDY structure



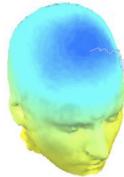
Choose a cluster: >> STUDY.cluster(**clust**)

```
>> STUDY.cluster
ans =
    27 total clusters
1x27 struct array with fields:
    name
    parent
    child
    comps
    sets
    algorithm
    centroid
    preclust
    topo
    topox
    topoy
    topoall
    topopol
```

ans =

```
    name: 'Cls 3'
    parent: {'ParentCluster 1'}
    child: []
    comps: [20 19 10 9 1 4]
    sets: [4x6 double]
    algorithm: {'Kmeans'    [25]}
    centroid: []
    preclust: [1x1 struct]
    selected: 1
    allinds: {4x1 cell} → 4 = # conditions
    setinds: {4x1 cell} → IC indices
    erspbase: {4x1 cell} → dataset indices
    erpdata: {4x1 cell}
    erptimes: [768x1 double]
        topo: [67x67 double]
        topox: [67x1 double]
        topoy: [67x1 double]
        topoall: {1x6 cell}
        topopol: [-1 1 -1 1 1 1]
        erspdata: {4x1 cell}
        erspfreqs: [1x126 double]
        ersptimes: [1x200 double]
```

Task 2: Understanding STUDY structure



```
>> STUDY.cluster(clust)
ans =
name: 'Cls 3'
    parent: {'ParentCluster 1'}
    child: []
    comps: [20 19 10 9 1 4]
    sets: [4x6 double]
algorithm: {'Kmeans' [25]}
centroid: []
preclust: [1x1 struct]
selected: 1
allinds: {4x1 cell} highlighted
setinds: {4x1 cell} highlighted
erspbase: {4x1 cell}
erpdata: {4x1 cell}
erptimes: [768x1 double]
topo: [67x67 double]
topox: [67x1 double]
topoy: [67x1 double]
topoall: {1x6 cell}
topopol: [-1 1 -1 1 1 1]
erspdata: {4x1 cell}
erspfreqs: [1x126 double]
ersptimes: [1x200 double]
```

```
>> STUDY.cluster(clust).setinds{cond}
```

```
ans =
```

14 38 46 50 54 54

Dataset 38!!

```
>> STUDY.cluster(clust).allinds{cond}
```

```
ans =
```

20 19 10 9 1 4

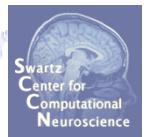
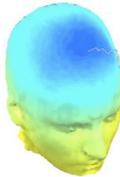
```
>> STUDY.datasetinfo(38) % access dataset 38
```

```
ans =
```

```
filepath: '.../Workshop/STUDY/S10'
filename: 'S10_attend1_pos5.set'
subject: 'S10'
session: 1
condition: 'NONTargAttnL'
group: 'normals'
index: 38
comps: [1 2 3 4 5 6 7 ...]
```



STUDY analysis, Part 1



Task 1

Script STUDY plotting functions

Task 2

STUDY structure details

Task 3

Load/plot data from commandline

Task 4

Apply significance limits

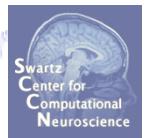
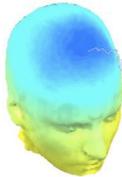
Task 5

Time/frequency analysis within cluster

Exercise...



Task 3: Load data from commandline



** Where is the raw data stored?

Data for each subject is stored in the file path
of that subject (STUDY.datasetinfo(subj).filepath)

** How to load it from the commandline:

File name format: 'setname.extension'

extension = '.ica*' or '.dat*' (for channel data)

for example:

S01_attend1_pos1.icaerp % ERP data

S01_attend1_pos1.icaersp % ERSP data

S01_attend1_pos1.icaitc % ITC data

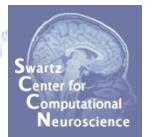
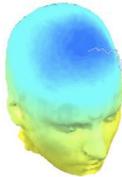
S01_attend1_pos1.icaspec % Power spectrum data

S01_attend1_pos1.icatopo % Scalp map data

% Example of channel data file name:

S01_attend1_pos1.daterp % ERP data

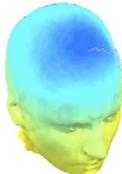
Task 3: Load individual ERSPs



```
% call in ERSP data for all ICs in a single cluster:  
  
clust = 5; % choose a cluster  
cond = 1; % choose experimental condition  
tmlims = [0 1000]; % time limits (ms)  
frqlims = [0 40]; % frequency limits (Hz)  
  
  
for ic = 1:size(STUDY.cluster(clust).sets,2)  
    setidx = STUDY.cluster(clust).setind{cond}(ic);  
    comp = STUDY.cluster(clust).allinds{cond}(ic);  
    [logersp(:,:,:,ic), logfreqs, timevals, params, baseersp] = ...  
        std_readersp(ALLEEG, setidx, comp, tmlims, frqlims);  
end;
```



Task 3: Load individual ERSPs



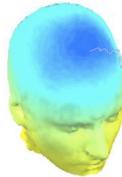
```
% Check imported variables in workspace:
```

```
>> whos logersp logfreqs timevals params baseersp
```

Name	Size	Bytes	Class
baseersp	91x1	728	double
logersp	91x106x7	540176	double
logfreqs	1x91	728	double
params	1x1	4432	struct
timevals	1x106	848	double



Task 3: PLOT individual ERSPs



```
% Plot the imported data:-----

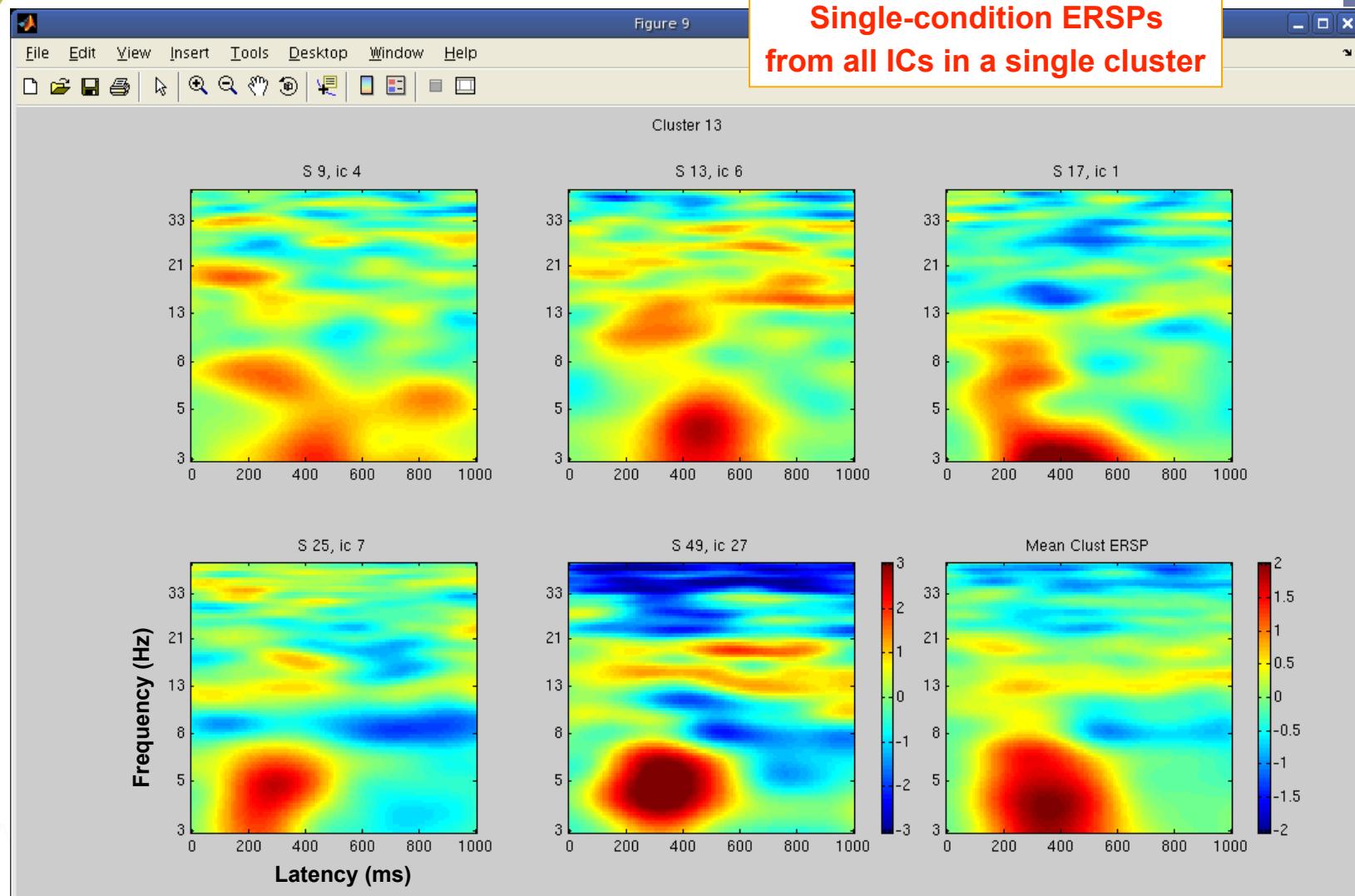
figure; clim = 3; % standardize color limits

for ic = 1:size(logersp,3)
    subplot(row,col,ic);
    imagesclogy(timevals, logfreqs, logersp(:,:,:ic)); % see tftopo
    set(gca,'clim', [-clim clim]); % adjust the color limits
    set(gca,'ydir','norm'); % plot low freqs at the bottom
end;

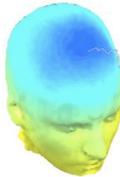
cbar; % include a colorbar

% plot the mean for comparison:
subplot(row,col,ic+1)
imagesclogy(timevals, logfreqs, mean(logersp,3));
```

Task 3: PLOT individual ERSPs



STUDY analysis, Part 1



Task 1

Script STUDY plotting functions

Task 2

STUDY structure details

Task 3

Load/plot data from commandline

Task 4

Apply significance limits

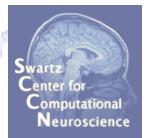
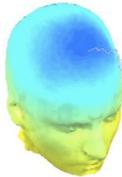
Task 5

Time/frequency analysis within cluster

Exercise...



Task 4: Requires access to .mat files



```
% Load ERSP data as a .mat file

% Variables:
cond = 1; % which experimental condition
subj = 1; % which subject

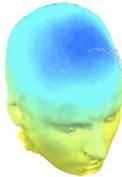
% files are all .mat format:
load_string = [basedir,subjs{subj}, '/', ...
               subjs{subj}, '_', setnames{cond}(1:end-4), '.icaersp'];

% actual string: '.../STUDY/S01/S01_attend1_pos1.icaersp'

ERSPdata = load('-mat',load_string);
```



Task 4: Raw data structure



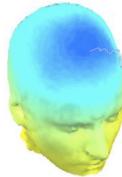
```
>> ERSPdata
```

ERSP dB data → comp1_ersp: [126x200 single]
dB baseline → comp1_erspbase: [1x126 single] → 200 time points
bootstrap limits → comp1_erspboot: [126x2 single] → upper and lower bootstrap limits
comp2_ersp: [126x200 single]
comp2_erspbase: [1x126 single] → 126 frequency bins
comp2_erspboot: [126x2 single]
126 frequency bins → freqs: [1x126 double]
200 time points → times: [1x200 double]
datatype: 'ERSP'
parameters: {1x26 cell}
datafile: [1x57 char]

```
>>
```



Task 4: ERSP significance limits



A blue line graph showing a continuous EEG signal with high-frequency noise, representing brain activity over time.

```
>> ERSPdata

comp1_ersp: [126x200 single]
comp1_erspbase: [1x126 single]
comp1_erspboot: [126x2 single] % (freqs x lower/upper limits)
%-----
% create min and max limit matrices:-----

minmask = repmat(ERSPdata.comp1_erspboot(:,1),...
[1 size(ERSPdata.comp1_ersp,2)]);

maxmask = repmat(ERSPdata.comp1_erspboot(:,2),...
[1 size(ERSPdata.comp1_ersp,2)]);

%-----
sig_ersp = ERSPdata.comp1_ersp; % extract relevant ERSP

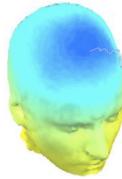
% zero out values within significance limits:-----
sig_ersp(find(sig_ersp > minmask & sig_ersp < maxmask)) = 0;

% plot the results:-----
figure; imagesclogy(ERSPdata.times, ERSPdata.freqs, sig_ersp);
%-----
```

A thick green arrow pointing horizontally to the right, indicating the continuation of the code or process.

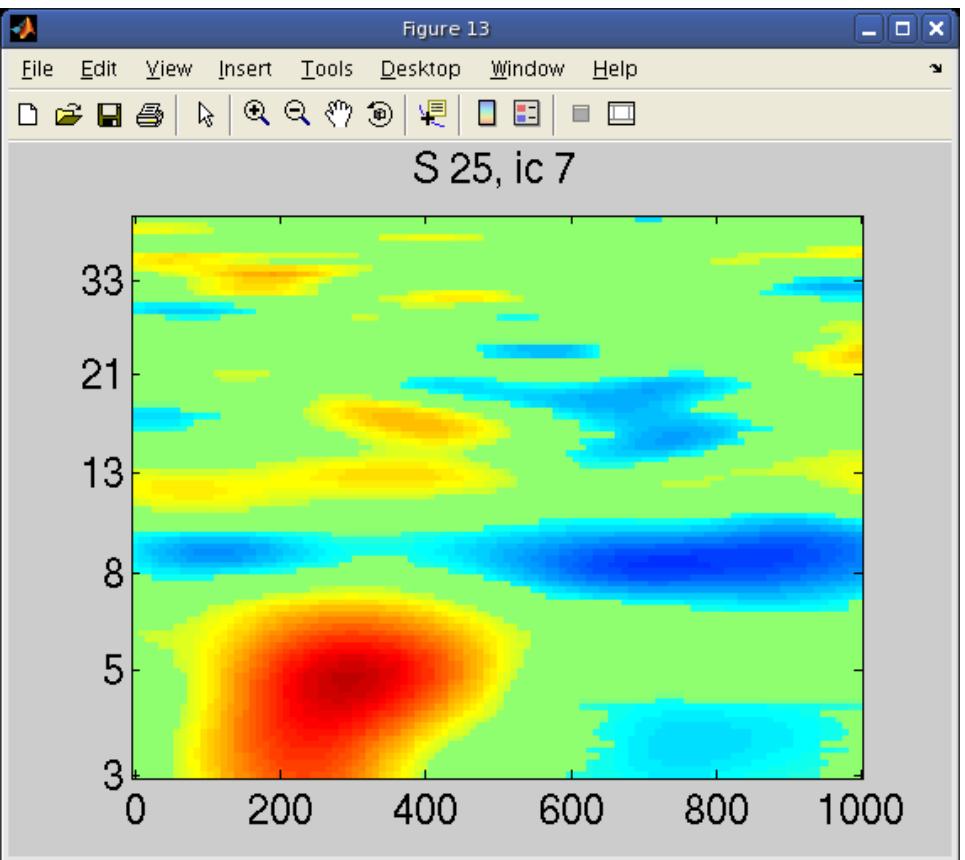
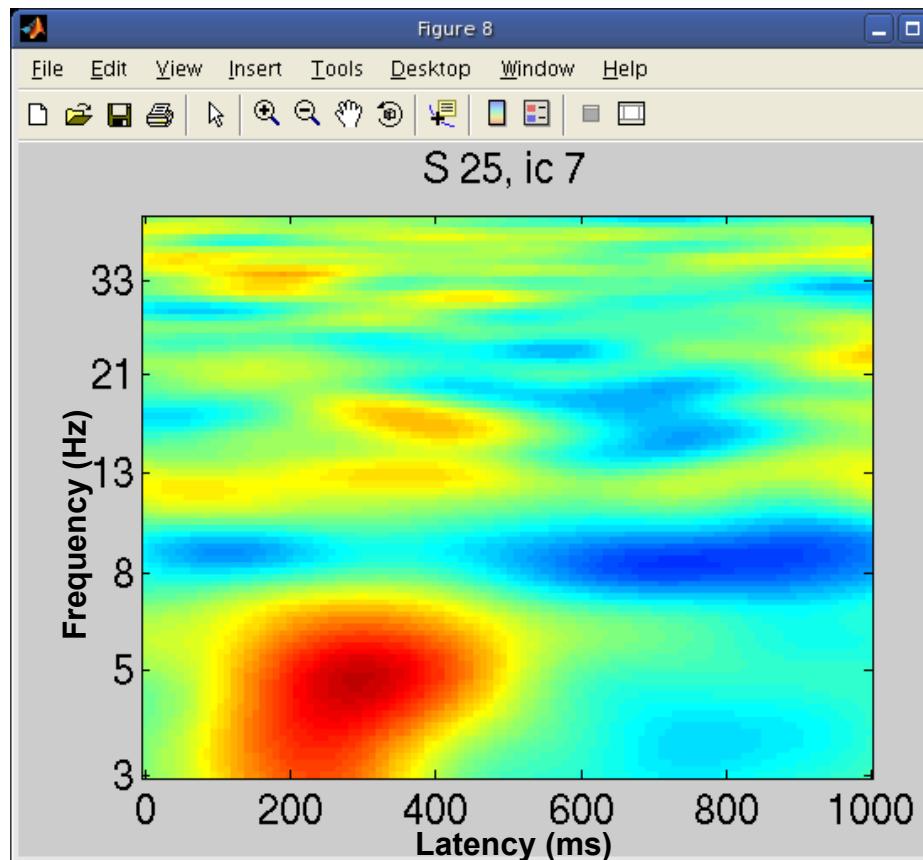


Task 4: Plot a single IC ERSP

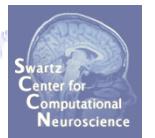
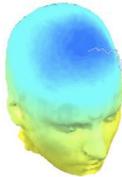


UN-masked

Masked ($p = .01$)



STUDY analysis, Part 1



Task 1

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Task 5

Time/frequency analysis within cluster

Exercise...



Task 5: Mean theta power across conditions

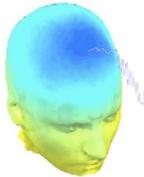


```
%%%%%%%%%%%%%%%
% Time/Frequency analysis:-----
%%%%%%%%%%%%%%%
clust = 13; % cluster to analyze
tlims = [250 500]; % time limits (ms)
flims = [3 6]; % frequency limits (Hz)

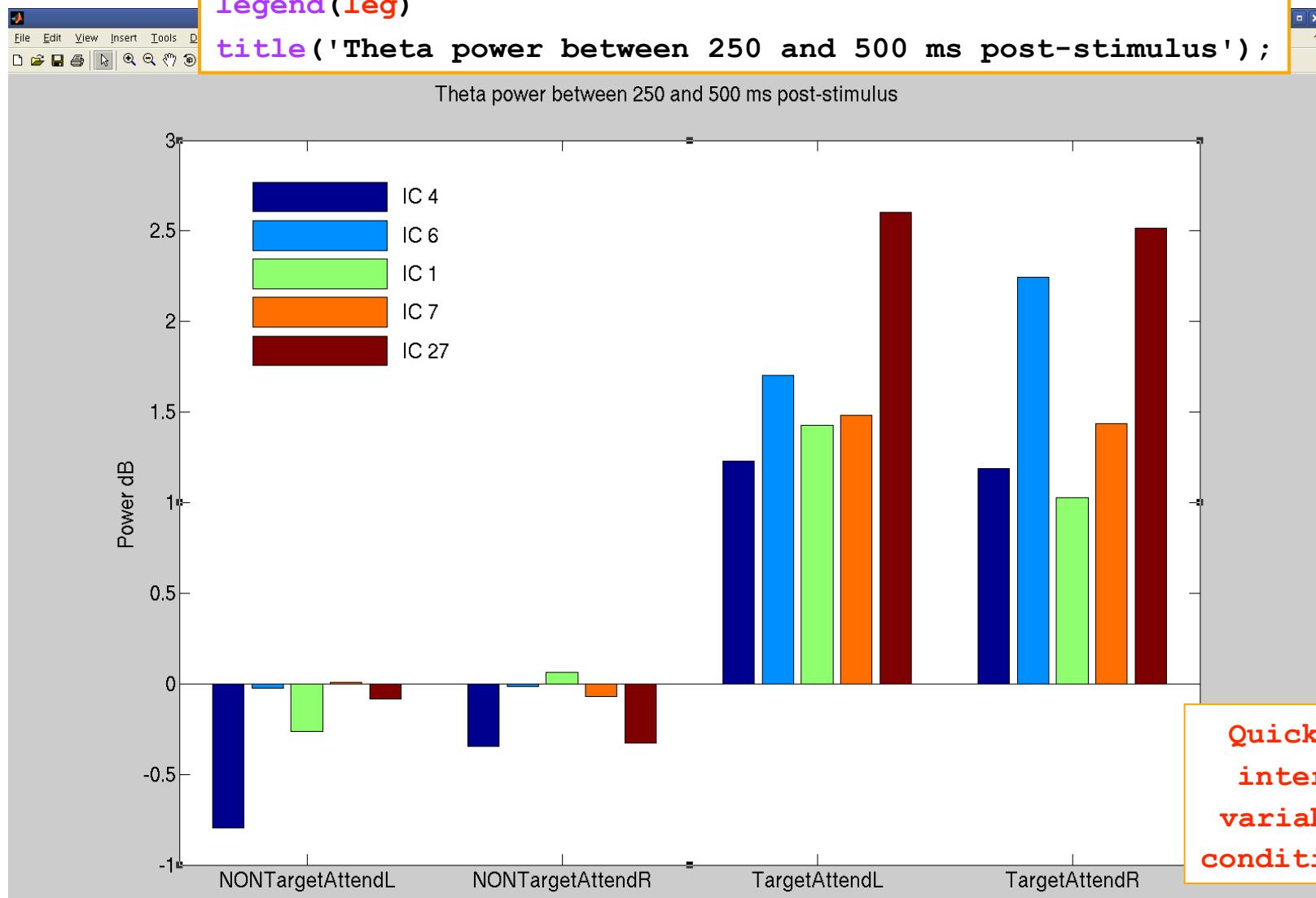
for cond = 1:4
    for ic = 1:length(STUDY.cluster(clust).comps)
        setidx = STUDY.cluster(clust).setinds{cond}(ic);
        comp = STUDY.cluster(clust).comps(ic);
        [logersp(:,:,ic), logfreqs, timevals, params, baseersp] = ...
        std_readersp(ALLEEG, setidx, comp, tlims, flims);
        tfdat(cond,ic) = mean(mean(logersp(:,:,ic)));
        leg{ic} = ['IC ',num2str(STUDY.cluster(clust).comps(ic))];
    end;
end;
```



Task 5: Mean theta power across conditions



```
figure;  
ph = bar([1:4],tfdat);  
set(gca,'xticklabel',STUDY.condition);  
legend(leg)  
title('Theta power between 250 and 500 ms post-stimulus');
```



Quickly assess
inter-subject
variability and
condition effects

Exercise



- 
- **Novice**
 - Script a loop through clusters to plot an activity measure(s) of your choice (ie, component properties, ERSP, spectra, ERP, etc)
 - use 'eegh' to recover EEGLAB plotting function commands
 - **Intermediate**
 - Plot an activity measure of your choice (ie, spectra, ERSPs, ITC, etc.) for all members of a cluster from the commandline:
 - Use `std_readersp()` or analogous STUDY function
 - **Advanced**
 - Plot masked ERSPs for all members of a cluster
 - use the `load ('-mat', load_string)` command
 - Plot mean power in a small time/frequency window across all ICs and conditions for a single cluster
- ** SCRIPT AVAILABLE ON THE COMMAND LINE
`practicum_10.m`
- 

